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(71) Applicants (for all designated States except US): CI-PHERGEN BIOSYSTEMS, INC. [US/US]; 6611 Dumbarton Circle, Freemont, CA 94555 (US). QUEEN ELIZABETH HOSPITAL [CN/CN]; 30 Gascoigne Road, Kowloon, Hong Kong SAR (CN).

(72) Inventors; and

(75) Inventors/Applicants (for US only): YIP, Timothy, Tak, Chun [CN/CN]; 1, Kapok Path, Westwood, Palm Springs, Yuen Long N.T., Hong Kong SAR (CN). CHO, Chi, Shing [—/CN]; Flat 9E, Block 4, The Tolo Place, Sunshine City, Ma On Shan, N.T., Hong Kong SAR (CN). AU, Siu, Kie [—/CN]; c/o Department of Clinical Oncology, Queen Elizabeth Hospital, 30 Gascoigne Road, Kowloon, Hong Kong SAR (CN). YIP, Tai-Tung [US/US]; 1532 Aster Court, Cupertino, CA 95014 (US). YIP, Christine, L. [US/US]; 1532 Aster Court, Cupertino, CA 95014 (US). YIP, Victor, F. [US/US]; 33008 Compton CT, Union City, CA 94587 (US).

(74) Agents: BENT, Stephen, A. et al.; Foley & Lardner, Washington Harbour, 3000 K Street, N.W. Suite 500, Washington, DC 20007-5101 (US).

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[Continued on next page]

(54) Title: SERUM BIOMARKERS IN LUNG CANCER

MARKER ID	MW	FRACTION	MARKER ID	MW	FRACTION	MARKER ID	MW	FRACTION	MARKER ID		FRACTION
IM-1	2011	· A	IM-37	3893	A	IM-72	54026	A	IM-109	2882	8
IM-2	2030	A	IM-38	3960	Α	IM-73 ·	60170	A	IM-110	2967	В
IM-3	2089	A	DM-39	3972	A	tM-75	74372	A	IM-111	2977	В
IM-4	2128	A	IM-40	3984	Α	IM-76	75545	A	IM-112	2994	8
1M-5	2148	A	IM-41	4066	Α	IM-77	77543	A	IM-113	3031	8
IM-6	2186	A	IM-42	4178	А	IM-78	79507	A	IM-114	3048	В
IM-7	2232	A	IM-43	4287	Α.	1M-79	89854	A	IM-115	3148	8
IM-8	2277	A	IM-44	4297	A	IM-80	101831	A	IM-116	3166	В
IM-9	2295	A	IM-45	4309	A	IM-81	104301	A	IM-117	3283	В
IM-10	2318	A	IM-46	4484	Α	1M-82	125160	A	IM-118	3308	В
IM-11	· 2411	A	IM-47	4649	Α	IM-83	132976	Α	IM-119	3332	В
IM-12	2434	A	IM-48	4798	Α	IM-84	149099	A	IM-120	3432	В
IM-13	2467	A	IM-49	5104	A	IM-85	2018		IM-121	3450	В
IM-14	2482	A	IM-50	5918	Α.	IM-86	2029	В	IM-122	3561	В
IM-15	2498	A	IM-51	6122	A	IM-87	2144		IM-123	3615	В
IM-16	2565	A	IM-52	6192		IM-88	2130		IM-124	3714	В
IM-17	2574	A	IM-53	6452	Α	IM-89	2168		IM-125	3730	В
IM-18	2586	A	IM-54	6660	A	IM-90	2184		IM-126	3834	В
IM-19	2605	A	IM-55	7768	Α	IM-91	2200		IM-127	3899	В
IM-20	2722	A	IM-56	8145	A	IM-92	2284		. IM-128	3969	В
IM-21	2746	A	IM-57	8954	A	IM-93	2299		IM-129	3986	В
IM-22	2788	A	IM-58	9312	Α	IM-94	2314	В	IM-130	3997	В
IM-23	2855	A	IM-59	9449	A	1M-95	2414		IM-131 ·	4013	В
IM-24	2871	A	(M-60	~10272	Α	IM-96	2428	В	IM-132	4181	В
IM-25	2984	A	IM-61	11663	A	IM-97	2451		IM-133	4297	В
IM-26	3030	Α	IM-62	13376	Α	IM-98	2468	В	IM-134	4311	В
IM-27	3144	A	IM-63	14698	A	IM-99	2483	В	IM-135	4465	В
IM-28	3243	A	IM-64	15190	Α	IM-100	2565	В	IM-136	4484	В
IM-29	3273	A	IM-64	68758	A	IM-101	2583	В	IM-137	4579	₿.
IM-30	3290	A	IM-65	15951	A	IM-102	2597	В	IM-138	4608	В
tM-31	3369	A	IM-66	15172	A	IM-103	2697	В	IM-139	4669	В
1M-32	3445	Α	IM-67	15925	A	IM-104	2715		IM-140	4747	В
IM-33	3483	A	IM-68	23436	Α	IM-105	2740		IM-141	4862	В
IM-34	3676	A	IM-69	39794	A	IM-106	2752	В	IM-142	4891	В
IM-35	3779	A	IM-70	44166	A	IM-107	2767	В	IM-143	5033	В
IM-38	3793	Α	IM-71	46890	A	IM-108	2865	В	IM-144	5077	В

(57) Abstract: Certain biomarkers and biomarker combinations are useful in a qualifying lung cancer status in a subject. A diagnostic methodology employing these biomarkers and combinations can detect whether a subject has lung cancer.



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SERUM BIOMARKERS IN LUNG CANCER

BACKGROUND OF THE INVENTION

[0001] The present invention relates generally to the field of serum biomarkers in lung carcinoma. More particularly, the invention relates to serum biomarkers that can distinguish lung cancer from normal.

[0002] Lung cancer is the leading cause of cancer death worldwide, resulting in 150,000 deaths per year in the United States. The mortality rate from lung cancer is greater than the combined mortality from breast, prostate and colorectal cancers. On the basis of morphology, lung cancer can be broadly classified into four main categories namely, adenocarcinoma, squamous cell carcinoma, large cell undifferentiated carcinoma and small cell carcinoma. In Hong Kong from 1990 to 1996, the proportions for adenocarcinoma, squamous cell carcinoma, large cell undifferentiated carcinoma and small cell carcinoma are 45.5%, 27.5%, 4.7% and 10.3% respectively. Both squamous cell carcinoma and small cell carcinoma are strongly associated with a smoking history.

[0003] Adenocarcinoma, squamous cell carcinoma, and large cell undifferentiated carcinoma are usually referred as "non-small cell carcinoma." They are relatively chemo-resistant, and hence the mainstay of treatment is surgery. By contrast, small cell carcinoma has a higher propensity for distant metastases and is mainly treated by chemotherapy.

[0004] Biopsy can be used to diagnose lung cancer, but it is an invasive procedure and, therefore, less than desirable. Other diagnostic methods for lung cancer include ultrasound and computed tomography (CT) scan.

[0005] It would be highly desirable to have a biomarker or combination of biomarkers capable of distinguishing between lung cancer and normal cells. In addition, a simple test could aid in tracking treatment progress and even identify molecular targets for therapy. The literature on lung cancer diagnosis has not disclosed heretofore such a biomarker or combination of biomarkers, however.

SUMMARY OF THE INVENTION

[0006] In accordance with the present invention, biomarkers and combinations of biomarkers are used to identify lung cancer. The method successfully distinguishes between lung cancer and normal states, and can be used to identify the particular type of lung cancer. In one embodiment, a method for qualifying lung carcinoma status in a subject (e.g., a patient) comprises analyzing a biological sample from the subject for one or more of the top 50 biomarkers as shown in Figure 2 or Figures 4A and 4B. Thus, to assess overall lung cancer risk versus normal, a biomarker is selected from the group consisting of

- (A) IM-522, IM-273, IM-520, IM-519, IM-454, IM-507, IM-521, IM-148, IM-266, IM-537, IM-471, IM-510, IM-544, IM-474, IM-155, IM-157, IM-176, IM-445, IM-177, IM-440, IM-468, IM-438, IM-547, IM-359, IM-436, IM-106, IM-455, IM-444, IM-158, IM-265, IM-50, IM-159, IM-156, IM-439, IM-157, IM-508, IM-514, IM-478, IM-473, IM-360, IM-435, IM-150, IM-151, IM-110, IM-51, IM-163, IM-437, IM-546, IM-153, and IM-268, or
- (B) WM-61, WM-447, WM-446, WM-133, WM-119, WM-278, WM-134, WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, WM-70, WM-369, WM-17, WM-473, WM-47, WM-203, WM-276, WM-279, WM-62, WM-366, WM-456, WM-428, WM-384, WM-287, WM-420, WM-292, WM-431, WM-455, WM-20, WM-340, WM-105, WM-389, WM-63, WM-354, WM-450, WM-466, WM-296, WM-343, WM-341, WM-339, WM-55, WM-66, WM-48, WM-38, WM-138, and WM-310,

[0007] wherein the biomarker is differentially present in samples of a subject with lung cancer and a so-called "normal" subject that is free of lung cancer.

[0008] More preferably, one or more of the top 15 biomarkers as shown in Figure 2 or Figures 4A and 4B is used to qualify lung cancer status. Thus, for assessing overall lung cancer status versus normal, the protein is selected from the group consisting of

- (A) IM-522, IM-273, IM-520, IM-519, IM-454, IM-507, IM-521, IM-148, IM-266, IM-537, IM-471, IM-510, IM-544, IM-474, IM-155, IM-471, IM-510, IM-544, IM-474, and IM-155, or
- (B) WM-61, WM-447, WM-446, WM-133, WM-119, WM-278, WM-134, WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, WM-70.
- [0009] Still more preferably, one or more of the top 5 biomarkers as shown in Figure 2 or Figures 4A and 4B is used to qualify lung cancer status. In this instance, for overall lung cancer status versus normal, the biomarker is selected from the group consisting of
- (A) IM-522, IM-273, IM-520, IM-519, and IM-454, or
- (B) WM-61, WM-447, WM-446, WM-133, and WM-119.
- [0010] In one embodiment, the method measures a plurality of biomarkers. The plurality of biomarkers can be measured simultaneously.
- [0011] Biomarkers that, by themselves, are able to identify lung cancer include the WM-446 and WM-447 protein biomarkers, and these are particularly preferred.
- [0012] The present invention also provides a method for qualifying lung cancer status in a subject (e.g., a patient), comprising (A) providing a spectrum generated by subjecting a biological sample from said subject to mass spectroscopic analysis that includes profiling on a chemically-derivatized affinity surface, and (B) putting the spectrum through pattern-recognition analysis that is keyed to at least one peak selected from the top 50 biomarkers as shown in Figure 2 or Figures 4A and 4B. Thus, for qualifying overall lung cancer status, the biomarker is selected from the, group consisting of
- (i) IM-522, IM-273, IM-520, IM-519, IM-454, IM-507, IM-521, IM-148, IM-266, IM-537, IM-471, IM-510, IM-544, IM-474, IM-155, IM-157, IM-176, IM-445, IM-177, IM-440, IM-468, IM-438, IM-547, IM-359, IM-436, IM-106, IM-455, IM-444, IM-158, IM-265, IM-50, IM-159, IM-156, IM-439, IM-157, IM-508, IM-514, IM-478, IM-473, IM-360, IM-435, IM-150, IM-151, IM-110, IM-51, IM-163, IM-437, IM-546, IM-153, and IM-268 or

(B) WM-61, WM-447, WM-446, WM-133, WM-119, WM-278, WM-134, WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, WM-70, WM-369, WM-17, WM-473, WM-47, WM-203, WM-276, WM-279, WM-62, WM-366, WM-456, WM-428, WM-384, WM-287, WM-420, WM-292, WM-431, WM-455, WM-20, WM-340, WM-105, WM-389, WM-63, WM-354, WM-450, WM-466, WM-296, WM-343, WM-341, WM-339, WM-55, WM-66, WM-48, WM-38, WM-138, and WM-310.

[0013] For assessing the overall lung cancer status, the pattern-recognition analysis may, for example, be paired to a pair of peaks selected from the group consisting of (A) IM-266 and IM-474, IM-266 and IM-38, IM-266 and IM-454, IM-266 and IM-522, IM- 266 and IM-544, IM-266 and IM-471, IM-474 and IM-151, IM-474 and IM-156, IM-474 and IM-544, IM-474 and IM-38, IM-522 and IM-507, IM-522 and IM-156, and IM-522 and IM-440;

or

- (B) WM-447 and WM-59, WM-447 and WM-19, WM-447 and WM-118, WM-447 and WM-473, WM-19 and WM-59, WM-19 and WM-473, WM-19 and WM-369, WM-61 and WM-154, WM-61 and WM-369, WM-118 and WM-59 and WM-282 and WM-127.
- [0014] More preferably, for assessing overall lung cancer status, the pattern-recognition analysis is keyed to a pair of peaks selected from the group consisting of (A) IM-266 and IM-474, IM-266 and IM-544, and IM-156 and IM-522; or
- (B) WM-447 and WM-59, WM-447 and WM-19, and WM-19 and WM-59. [0015] Alternatively, the pattern-recognition analysis for assessing overall lung cancer status may be keyed to a triplet of peaks selected from the group consisting of (A) IM-266, IM-454 and IM-474; and IM-266, IM-474 and IM-544; or
- (B) WM-447, WM-19 and WM-473.

[0016] In other embodiments, the pattern-recognition analysis may be keyed to a combination of more than three peaks, more particularly to a combination of 4, 5 or 6 peaks, where the combination is selected from among the combinations shown in Tables 1 and 2 herein.

[0017] In each case, the biomarker is differentially present in samples of a subject with lung cancer and a normal subject.

[0018] The invention also contemplates a kit for detecting and diagnosing lung cancer, thereby to assess lung cancer status. Kits within the invention comprise, for example, (i) an adsorbent attached to a substrate that retains one or more of the biomarkers shown in Figure 2 or Figures 4A and 4B, and (ii) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent. An inventive kit may further comprise a washing solution and/or instructions for making a washing solution. The kits may include more than type of adsorbent, each present on a different substrate, e.g., on a WCX and IMAC biochip. In addition, the kits may comprise one or more containers with biomarker samples, to be used as standard(s) for calibration. The substrate comprising the adsorbent may be designed to engage a probe interface and, hence, function as a probe in gas phase ion spectrometry, preferably mass spectrometry. Alternatively, the kit may further comprise a second substrate adapted to engage the probe interface, on which the substrate comprising the adsorbent is mounted. [0019] The method and kit according to the invention produce an article of manufacture in which one or more biomarkers according to the invention are bound to an adsorbent, optionally contacted with a matrix or energy absorbing molecule. [0020] The present invention also provides software for qualifying lung carcinoma status in a subject, comprising an algorithm for analyzing data extracted from a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, wherein said data relates to one or more biomarkers according to the invention. In one embodiment, the algorithm carries out a pattern-recognition analysis that is keyed to data relating to at least one of the biomarkers. In another embodiment, the algorithm comprises classification tree analysis that is keyed to data relating to at least one of the biomarkers. In yet another embodiment, the algorithm

comprises an artificial neural network analysis that is keyed to data relating to at least one of the biomarkers.

[0021] In certain embodiments, the present invention provides methods and kits that use serum amyloid a protein or a fragment thereof to qualify lung carcinoma status in a subject. In one of these embodiments, the serum amyloid a biomarker has an apparent molecular weight of about 2803, 3168, 3277, 3552, 3897, 4300, 4490, 4655, 5927, 6874, 7776, 7941, 8152, 8952, 9233, 10300, 10866, or 10851 Daltons. In another embodiment, the serum amyloid a biomarker has an apparent molecular weight of about 3168, 3277, 3552, 3897, 4300, 4490, 4655, 7776, 7941, 8152, 8952, or 10851 Daltons. In yet another embodiment, the serum amyloid a biomarker has an apparent molecular weight of about 11.5 to 11.7 kD.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022] Figures 1A-1D show all biomarkers identified with a Cu(II) IMAC3 ProteinChip® array format.

[0023] Figure 2 shows the top 50 biomarkers identified with a Cu(II) IMAC3 ProteinChip® array format.

[0024] Figures 3A-3O show all biomarkers identified with a WCX ProteinChip® array format.

[0025] Figures 4A and 4B show the top 50 biomarkers identified with a WCX ProteinChip® array format.

[0026] Figure 5 shows fragments of serum amyloid A (SAA) that are biomarkers according to the present invention.

[0027] Figure 6 shows identification of SAA biomarkers with an anti-SAA antibody.

[0028] Figures 7-16 are spectra from WCX chips in which all of the top 15 WCX marker peaks are labeled, along with various other peaks from among the top 50 WCX peaks. Red shows spectra from lung cancer patients and gray shows normals.

[0029] Figures 17-28 are spectra from IMAC chips in which all of the top 15 WCX marker peaks are labeled, along with various other peaks from among the top 50 IMAC peaks. Blue shows spectra from lung cancer patients and gray shows normals.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

[0030] In accordance with the present invention, a series of biomarkers associated with lung cancer has been discovered. In the present context, a biomarker is an organic biomolecule, particularly a polypeptide or protein, which is differentially present in a sample taken from a subject having lung cancer as compared to a comparable sample taken from a normal subject. A biomarker also may be differentially present in a sample taken from a subject with one type of lung cancer, e.g., small cell carcinoma, as compared to a comparable sample taken from a subject with a different type of lung cancer, e.g., adenocarcinoma or squamous cell carcinoma, or differentially present at different stages of a type of lung cancer. A biomarker is differentially present in samples taken from two groups of subjects if it is present at an elevated level or a decreased level in samples of the first group as compared to samples of the second group. More particularly, a biomarker is a polypeptide that is characterized by an apparent molecular weight, as determined by mass spectrometry, and that is present in samples from lung cancer subjects in an elevated or decreased level, as compared to subjects that do not have lung cancer. A biomarker is differentially present between two sets of samples if the amount of the biomarker in one sample set differs in a statistically significant way (p < 0.01) from the amount of biomarker in the other sample set.

[0031] The biomarkers of the invention can be used to assess lung cancer status in a subject. For example, they are capable of identifying lung cancer and successfully distinguishing it from normal subjects, thereby providing a way of diagnosing the presence or absence of lung cancer, including the presence or absence of a particular kind of lung cancer. In addition, the biomarkers are useful in assessing the risk of developing lung cancer, in staging of lung cancer and in assessing the effectiveness of treatment. Thus, "lung cancer status" in the context of the present invention includes, inter alia, the presence or absence of disease, the risk of developing disease, the stage of the disease, and the effectiveness of treatment of disease. Based on this status, further procedures may be indicated, including additional diagnostic tests or therapeutic procedures or regimens, such as endoscopy, biopsy, surgery, chemotherapy, immunotherapy, and radiation therapy.

[0032] In some instances, a single biomarker is capable of identifying lung cancer with a sensitivity or specificity of at least 85%, whereas, in other instances, a combination or plurality of biomarkers is used to obtain a sensitivity or specificity of at least 85%. The biomarkers and combinations of biomarkers thus can be used to qualify lung cancer status in a subject or patient.

[0033] The biomarkers according to the invention are present in serum. The biological sample used according to the present invention, however, need not be a serum sample. Thus, a biological sample for qualifying lung cancer status may be a serum, plasma or blood sample, although serum samples are preferred.

[0034] All of the biomarkers are characterized by molecular weight. A list of all the biomarkers obtained with the Cu(II) IMAC3 ProteinChip® array (Ciphergen Biosystems, Inc., Fremont, California, USA) is provided in Figures 1A-1D, and Figure 2 lists the top 50 biomarkers that distinguish between lung cancer and normal subjects that are identified by Cu(II) IMAC3 protocol described herein. Figures 3A-3O comprise a list of all the biomarkers obtained with the WCX2 ProteinChip® array, and Figures 4A and 4B comprise a ranking of the top 50 biomarkers that distinguish between (i) lung cancer and normal subjects, (ii) subjects with each of four types of lung cancer and normal subjects, and (iii) two types of lung cancer, e.g., adenocarcinoma versus squamous cell carcinoma, as identified by WCX2 protocol described herein.

[0035] The top 50 biomarkers were determined by decision tree analysis using Biomarker PatternsTM software from Ciphergen Biosystems, Inc. Biomarkers other than those within the top 50 also are useful in distinguishing between subjects with lung cancer and normal subjects and may, in particular, appear in decision trees with multiple nodes. In preferred embodiments, one or more of the top 15 biomarkers are used, and in even more preferred embodiments, one or more of the top 5 biomarkers are used.

[0036] In each of Figures 1A-1D and 3A-3O, the number in the first column is the biomarker identifier. Thus, the first row in Figures 1A-1D relates to biomarker IM-1, the second row relates to biomarker IM-2, and so forth ("IM-" denoting biomarkers identified with the IMAC chip). Similarly, the first row in Figures 3A-3O relates to

biomarker WM-1 and the second row relates to biomarker WM-2 ("WM-" denoting biomarkers identified with the WCX2 chip). The number in the second column in Figures 1A-1D is the apparent molecular weight of the biomarker in daltons, as determined by mass spectrometry. In Figures 3A-3O, the apparent molecular weights for the biomarkers identified in the first column are reported in columns 3 through 11. The letter in the second column of Figures 1A-1D and the third column of Figures 3A-3O denotes the fraction in which the biomarker elutes in the protocol described herein; that is, biomarkers with an "A" elute in the first fraction, biomarkers with a "B" elute in the second fraction, and so forth. The fraction in which the biomarker elutes correlates with its pI, which biomarkers eluting at higher pH having a higher pI, and biomarkers eluting at lower pH having a lower pI.

[0037] Presenting the mass and affinity characteristics of a given biomarker within the invention, as in this description, characterizes that biomarker so as allow one to obtain and measure it, in accordance with the teachings herein. If desired, any of the biomarkers can be sequenced, in order to obtain an amino acid sequence, but this is not required to practice the present invention.

[0038] For example, a biomarker can be peptide mapped with a number of enzymes, such as trypsin and V8 protease, and the molecular weights of the digestion fragments can be used to search databases for sequences that match the molecular weights of the digestion fragments generated by the various enzymes. Alternatively, if the biomarkers are not proteins included in known databases, degenerate probes can be made based on the N-terminal amino acid sequence of the biomarker, which then are used to screen a genomic or cDNA library created from a sample from which the biomarker was initially detected. The positive clones can be identified, amplified, and their recombinant DNA sequences can be subcloned using techniques which are well known. Finally, protein biomarkers can be sequenced using protein ladder sequencing. Protein ladders can be generated by fragmenting the molecules and subjecting fragments to enzymatic digestion or other methods that sequentially remove a single amino acid from the end of the fragment. The ladder is then analyzed by mass spectrometry. The difference in masses of the ladder fragments identifies the amino acid removed from the end of the molecule.

[0039] Several biomarkers identified in accordance with the teachings of the present invention fit to serum amyloid A (SAA) or to a fragment of SAA. SAA is a well-known acute phase inflammatory marker. A number of the SAA biomarkers are identified in Figure 5 by both molecular mass and amino acid sequence. Most of these markers bound anti-SAA antibodies, as shown in Figure 6. The intact mass of SAA is 11.5 to 11.7 kD, and these biomarkers also have been identified by the present methodology. Fragments preferably have a molecular mass of at least about 200 Daltons, more preferably at least about 500 Daltons. In even more preferred embodiments, fragments have a molecular mass of at least about 800 Daltons, and most preferably at least about 1 Kilodalton.

[0040] In one embodiment, the fragments of SAA include a sequence of amino acids that is recognized by an epitope of an anti-SAA antibody. One way of identifying suitable fragments for use in the present invention is to enzymatically digest SAA and test the resulting fragments for the ability to bind to an anti-SAA antibody. Fragments that bind anti-SAA antibody can be sequenced using techniques well-known in the art, although the sequence of the fragment is not needed to practice the invention. In order to practice the invention with a fragment from the enzymatic digest that is identified as binding anti-SAA antibody, all that is required is to subject to the fragment to mass spectrometry to determine its mass.

[0041] The serum biomarkers according to the present invention were identified by comparing mass spectra of samples derived from sera from two groups of newly-diagnosed subjects, subjects with lung cancer and normal subjects. The subjects were diagnosed according to standard clinical criteria. Lung cancer subjects were histologically confirmed, and subjects without lung cancer were followed for at least 18 months following serum collection for any sign of lung cancer, to exclude subjects with asymptomatic lung cancer.

[0042] Sera from each group of subjects was collected, and fractionated with Q Ceramic HyperDF ion exchange resin (Biosepra SA, France) into six fractions which eluted at different pH. Fraction A comprised the flow through plus pH 9 eluant, Fraction B comprised the pH 7 eluant, Fraction C comprised the pH 5 eluant, Fraction D comprised the pH 4 eluant, Fraction E comprised the pH 3 eluant, and Fraction F

comprised isopropyl alcohol/acetonitrile TFA eluant. Fractions A through F are identified on Figures 7-28 as Fractions 1 through 6, respectively.

[0043] Each fraction was diluted and applied to a ProteinChip® array, either a Cu(II) IMAC3 or WCX2 chip array. Both of these chip arrays are produced by Ciphergen Biosystems, Inc. (Fremont, CA).

[0044] The Cu(II) IMAC3 is an "immobilized metal affinity-capture" chip, with a nitrilotriacetic acid surface for high-capacity copper binding and subsequent affinity capture of proteins with metal binding residues. Imidazole may be used in binding and washing solutions to moderate protein binding, including binding of non-specific proteins. Increasing the concentration of imidazole in the washing buffers reduces the binding of the target proteins. It is produced by photopolymerizing 5-methylacylamido-2-(N,N-biscarboxymethylamino)pentanoic acid (7.5 wt%) and N,N'-methylenebisacrylamide (0.4 wt%) using (-) riboflavin (0.02 wt%) as a photoinitiator. The monomer solution is deposited onto the chip substrate and irradiated to photopolymerize. The chip then is activated with Cu(II).

[0045] The WCX2 is a weak cation exchange array with a carboxylate surface to bind cationic proteins. The negatively charged carboxylate groups on the surface of the WCX2 chip interact with the positive charges exposed on the target proteins. The binding of the target proteins is reduced by increasing the concentration of salt or by increasing the pH of the washing buffers.

[0046] Following application of the eluant fraction, the chips were incubated to allow the polypeptides in the eluant to bind to the sites on the chip by an affinity interaction. After incubation, each chip array was washed to remove polypeptides that bind non-specifically and buffer contaminants. That chip then was dried, and an energy absorbing molecule or matrix was applied to it, to facilitate desorption and ionization in a mass spectrometer.

[0047] In the mass spectrometer, retained polypeptides were desorbed from the chip array by laser desorption and ionization in a ProteinChip® Reader, which is integrated with ProteinChip® Software and a personal computer to analyze proteins captured on chip arrays. The ion optic and laser optic technologies in the ProteinChip® Reader detects proteins ranging from small peptides of less than 1000 Da up to proteins of

300 kilodaltons or more, and calculates the mass based on time-of-flight. Ionized polypeptides were detected and their mass accurately determined by this Time-of-Flight (TOF) Mass Spectrometry.

[0048] The mass spectra obtained for each group were subjected to scatter plot analysis, to eliminate run-to-run variation. Protein clusters on the scatter plot that had the same pattern for both lung cancer and normal subjects, *i.e.*, protein clusters that were either elevated in both groups of subjects or depressed in both groups of subjects, were eliminated as potential biomarkers. The remaining polypeptides were further analyzed for their ability to accurately identify subjects with lung cancer. Because the molecular weights were derived from scatter plot analysis, and because of limits on the ability of mass spectrometry to resolve molecular weights, the "absolute" molecular weight values given in Figures 1A-1D and 3A-3O actually represent approximate molecular weights.

[0049] The biomarkers of this invention are characterized by their mass-to-charge ratio as determined by mass spectrometry. The mass-to-charge ratio of each biomarker is provided in Figures 1A-1D and 3A-3O. For example, IM-1 in Figure 1A has a measured mass-to-charge ratio of 2011. The mass-to-charge ratios were determined from mass spectra generated on a Ciphergen Biosystems, Inc. PBS II mass spectrometer. This instrument has a mass accuracy of about +/- 0.15 percent. Additionally, the instrument has a mass resolution of about 400 to 1000 m/dm, where m is mass and dm is the mass spectral peak width at 0.5 peak height. The mass-to-charge ratio of the biomarkers was determined using Biomarker WizardTM software (Ciphergen Biosystems). Biomarker Wizard assigns a mass-to-charge ratio to a biomarker by clustering the mass-to-charge ratios of the same peaks from all the spectra analyzed, as determined by the PBSII, taking the maximum and minimum mass-to-charge-ratio in the cluster, and dividing by two. Accordingly, the masses provided reflect these specifications.

[0050] The biomarkers of this invention are further characterized by the shape of their spectral peak in time-of-flight mass spectrometry. Mass spectra showing peaks representing the biomarkers are presented in Figures 7-28. The biomarker identifier numbers from Figures 2 and 4A-4B, respectively, are shown next to the peak, along

with their rank, which is indicated in parentheses below the biomarker identifier number.

[0051] The biomarkers of this invention are further characterized by their binding properties on chromatographic surfaces. Most of the biomarkers bind to IMAC (Cu) or WCX adsorbents (e.g., the Ciphergen® IMAC (Cu) or WCX ProteinChip® arrays) after washing as described herein.

[0052] Thus, a given molecular weight for a biomarker herein should be interpreted as the midpoint of a molecular-weight range. The accuracy of the mass spectrometer is +/- 0.15%, and the actual molecular weight for a biomarker is therefore the value given, +/- 0.15%. For example, the actual molecular weight for biomarker IM-273 is 11705 +/- 0.15%, or between 11687 and 11722. Often, the range surrounding the "absolute" value given in the figure is no more than +/- 5 daltons (2006 to 2016 for IM-1), generally no more than +/- 3 daltons (2008 to 2014 for IM-1), and often as small as +/- 1 dalton (2010 to 2012 daltons for IM-1).

[0053] CART® (Salford Systems, San Diego, CA), a classification and regression tree software, was used to determine whether a potential biomarker had predictive value in assessing lung cancer. A software macro randomly selected a subset of 15% of the peaks from Figures 1A-1D or Figures 3A-3O. The peaks and peak heights from each sample were provided to the CART® software for analysis. The software performed an iterative analysis until a single decision tree was generated that was capable of distinguishing between cancerous and non-cancerous. Each node in the resulting decision tree sorted based on the peak height of a single biomarker. A tree may contain any number of nodes, but generally contains from 1 to 6 nodes. From a practical standpoint in a commercial diagnostic test, a decision tree with fewer nodes is preferred. A total of 2000 decision trees, each based on a different 15% subset of the peaks from Figures 1A-1D or Figures 3A-3O, were generated.

[0054] The CART® software assigned a score to each biomarker in the subset, based on its relative importance. A score of 100 is very high and a score of 0 is very low. The CART® software also determined the sensitivity and specificity of each decision tree.

[0055] The data generated by the decision tree analysis was subjected to further analysis. The biomarkers were ranked based on their average scores, which were determined by adding up a biomarker's scores for each decision tree in which it appeared, and dividing by the total number of decision trees in which the biomarker appeared. Approximately 500 of the potential biomarkers showed up in at least one tree, and most of the biomarkers showed up in about 150 to 400 of the two thousand trees. The top 50 biomarkers for the IMAC and WCX chip arrays as determined by this method are shown in Figures 2 and 4A-4B, respectively.

[0056] All of the trees having sensitivities and specificities greater than 85% also were identified. All trees capable of distinguishing lung cancer from normal and having from 1 to 6 nodes that meet the 85/85 criterion are shown in Tables 1 and 2.

TABLE 1. Decision trees with IMAC Biomarkers.

·	2 trees 2 trees				
·					
·					
	2 trees				
474					
474					
1					
153					
156					
113					
401					
474					
153					
474					
4 Nodes					
508	251				
	153 156 113 401 474 153	156 113 401 474 153 474			

266	544	474	493		
266	157	126	420		
266	544	474	482		
266	471	474	38		
266	544	474	38		
266	514	471	203		
522	58	266	474		
5 Nodes					
266	544	473	151	437	
266	454	474	153	264	
273	143	544	401	199	

TABLE 2. Decision Trees with WCX Biomarkers.

1 Node				
446				
447				
2 Node	S			
282	127			
3 Node	S			
61	16	27		
61	119	154		
61	120	154		
61	369	184	-	
61	184	129		
61	19	282		
133	282	319		
282	59	218		
282	111	65		

446	19	16			
4 Node	s				
61	369	282	184		
61	48	203	3		
446	369	111	67		
446	466	58	120		
446	19	59	113		
446	282	19	47		
447	118	59	417		
447	118	59	473		
447	65	59	275		
447	19	59	282		
447	369	59	206		
447	19	59	253		
447	19	47	70		
5 Node					
61	369	128	184	197	
61	17	425	366	341	
133	139	363	216	273	
282	133	48	19	253	
369	310	19	109	384	
446	282	15	319	66	
447	19	71	473	31	
447	19	17	473	438	
447	47	31	365	59	
6 Nod	es				
369	366	192	471	19	439

[0057] Each of the biomarker combinations of Tables 1 and 2 are preferred combinations for distinguishing lung cancer subjects from normal subjects in accordance with the present invention.

[0058] All biomarkers that appeared in at least two of the trees that met the 85/85 criterion were identified. For these biomarkers, Tables 3 and 4 provide the number of times the biomarker occurred in a trees that met the criterion, as well as the ranking of that biomarker on the top 50 lists of Figures 2 and 4A-4B.

TABLE 3. Correlation of IMAC biomarker decision tree frequencies and ranking.

Peak	# times	Rank	
266	9	9	
522	8	1	
474	4	14	
520	2	3	
148	1	8	
273	1	2	

TABLE 4. Correlation of WCX biomarker decision tree frequencies and ranking.

Peak	# times	Rank
447	11	2
61	10	1
446	7	3
282	4	9
369	2	. 8
133	2	4

[0059] Biomarkers that occurred frequently in the highly discriminatory trees occurred among the top 50 ranked biomarkers, and typically had a top 10 ranking. In addition, certain pairs of biomarkers reappear, e.g., WM-447 and WM-59, WM-447 and WM-19, WM-19 and WM-59, IM-266 and IM-474, IM-266 and IM-38, IM-266 and IM-454, IM-522 and IM-266. There also are repeats among triplets of biomarkers, such as IM-266, IM-266 and IM-38, and WM-447, WM-19 and WM-473. Other repeating pairs and trios of biomarkers can be seen in Tables 3 and 4, and are preferred.

[0060] Biomarkers and combinations of biomarkers identified in accordance with the present description may be used to qualify lung cancer status in a subject. In particular, a biomarker or combination of biomarkers can be used to distinguish lung cancer patients from normal patients with a high degree of specificity or sensitivity, i.e., greater than at least 85%, preferably greater than at least 90%, and more preferably greater than 95%.

[0061] According to one aspect of the invention, therefore, the detection of biomarkers for diagnosis of lung cancer status entails contacting a sample from a subject with a substrate, e.g., a SELDI probe, having an adsorbent thereon, under conditions that allow binding between the biomarker and the adsorbent, and then detecting the biomarker bound to the adsorbent by gas phase ion spectrometry, for example, mass spectrometry. Other detection paradigms that can be employed to this end include optical methods, electrochemical methods (voltametry and amperometry techniques), atomic force microscopy, and radio frequency methods, e.g., multipolar resonance spectroscopy. Illustrative of optical methods, in addition to microscopy, both confocal and non-confocal, are detection of fluorescence, luminescence, chemiluminescence, absorbance, reflectance, transmittance, and birefringence or refractive index (e.g., surface plasmon resonance, ellipsometry, a resonant mirror method, a grating coupler waveguide method or interferometry).

[0062] In one aspect, the markers of this invention are detect by gas phase ion spectrometry, which refers to the use of a gas phase ion spectrometer to detect gas phase ions. A gas phase ion spectrometer is an apparatus that detects gas phase ions. Gas phase ion spectrometers include an ion source that supplies gas phase ions. Gas

phase ion spectrometers include, for example, mass spectrometers, ion mobility spectrometers, and total ion current measuring devices.

[0063] "Mass spectrometer" refers to a gas phase ion spectrometer that measures a parameter which can be translated into mass-to-charge ratios of gas phase ions. Mass spectrometers generally include an ion source and a mass analyzer. Examples of mass spectrometers are time-of-flight, magnetic sector, quadrupole filter, ion trap, ion cyclotron resonance, electrostatic sector analyzer and hybrids of these. "Mass spectrometry" refers to the use of a mass spectrometer to detect gas phase ions. "Laser desorption mass spectrometer" refers to a mass spectrometer which uses laser as a means to desorb, volatilize, and ionize an analyte.

[0064] "Mass analyzer" refers to a sub-assembly of a mass spectrometer that comprises means for measuring a parameter which can be translated into mass-to-charge ratios of gas phase ions. In a time-of flight mass spectrometer the mass analyzer comprises an ion optic assembly, a flight tube and an ion detector.

[0065] "Ion source" refers to a sub-assembly of a gas phase ion spectrometer that provides gas phase ions. In one embodiment, the ion source provides ions through a desorption/ionization process. Such embodiments generally comprise a probe interface that positionally engages a probe in an interrogatable relationship to a source of ionizing energy (e.g., a laser desorption/ionization source) and in concurrent communication at atmospheric or subatmospheric pressure with a detector of a gas phase ion spectrometer.

[0066] Forms of ionizing energy for desorbing/ionizing an analyte from a solid phase include, for example: (1) laser energy; (2) fast atoms (used in fast atom bombardment); (3) high energy particles generated via beta decay of radionucleides (used in plasma desorption); and (4) primary ions generating secondary ions (used in secondary ion mass spectrometry). The preferred form of ionizing energy for solid phase analytes is a laser (used in laser desorption/ionization), in particular, nitrogen lasers, Nd-Yag lasers and other pulsed laser sources. "Fluence" refers to the laser energy delivered per unit area of interrogated image. Typically, a sample is placed on the surface of a probe, the probe is engaged with the probe interface and the probe

surface is struck with the ionizing energy. The energy desorbs analyte molecules from the surface into the gas phase and ionizes them.

[0067] Other forms of ionizing energy for analytes include, for example: (1) electrons which ionize gas phase neutrals; (2) strong electric field to induce ionization from gas phase, solid phase, or liquid phase neutrals; and (3) a source that applies a combination of ionization particles or electric fields with neutral chemicals to induce chemical ionization of solid phase, gas phase, and liquid phase neutrals.

[0068] A preferred mass spectrometric technique for use in the invention is Surface Enhanced Laser Desorption and Ionization (SELDI), as described, for example, in U.S. patents No. 5,719,060 and No. 6,225,047, both to Hutchens and Yip, in which the surface of a probe that presents the analyte (here, one or more of the biomarkers) to the energy source plays an active role in desorption/ionization of analyte molecules. In this context, "probe" refers to a device adapted to engage a probe interface and to present an analyte to ionizing energy for ionization and introduction into a gas phase ion spectrometer, such as a mass spectrometer. A probe typically includes a solid substrate, either flexible or rigid, that has a sample-presenting surface, on which an analyte is presented to the source of ionizing energy.

[0069] One version of SELDI, called Surface-Enhanced Affinity Capture" or "SEAC," involves the use of probes comprised of a chemically selective surface ("SELDI probe"). A "chemically selective surface" is one to which is bound either the adsorbent, also called a "binding moiety" or "capture reagent," or a reactive moiety that is capable of binding a capture reagent, e.g., through a reaction forming a covalent or coordinate covalent bond.

[0070] The phrase "reactive moiety" here denotes a chemical moiety that is capable of binding a capture reagent. Epoxide and carbodiimidizole are useful reactive moieties to covalently bind polypeptide capture reagents such as antibodies or cellular receptors. Nitriloacetic acid and iminodiacetic acid are useful reactive moieties that function as chelating agents to bind metal ions that interact non-covalently with histidine containing peptides. A "reactive surface" is a surface to which a reactive moiety is bound. An "adsorbent" or "capture reagent" can be any material capable of

binding a biomarker of the invention. Suitable adsorbents for use in SELDI, according to the invention, are described in U.S. patent No. 6,225,047, supra. [0071] One type of adsorbent is a "chromatographic adsorbent," which is a material typically used in chromatography. Chromatographic adsorbents include, for example, ion exchange materials, metal chelators, immobilized metal chelates, hydrophobic interaction adsorbents, hydrophilic interaction adsorbents, dyes, simple biomolecules (e.g., nucleotides, amino acids, simple sugars and fatty acids), mixed mode adsorbents (e.g., hydrophobic attraction/electrostatic repulsion adsorbents). "Biospecific adsorbent" is another category, for adsorbents that contain a biomolecule, e.g., a nucleotide, a nucleic acid molecule, an amino acid, a polypeptide, a polysaccharide, a lipid, a steroid or a conjugate of these (e.g., a glycoprotein, a lipoprotein, a glycolipid). In certain instances the biospecific adsorbent can be a macromolecular structure such as a multiprotein complex, a biological membrane or a virus. Illustrative biospecific adsorbents are antibodies, receptor proteins, and nucleic acids. A biospecific adsorbent typically has higher specificity for a target analyte than a chromatographic adsorbent.

[0072] Another version of SELDI is Surface-Enhanced Neat Desorption (SEND), which involves the use of probes comprising energy absorbing molecules that are chemically bound to the probe surface ("SEND probe"). The phrase "Energy absorbing molecules" (EAM) denotes molecules that are capable of absorbing energy from a laser desorption ionization source and, thereafter, contributing to desorption and ionization of analyte molecules in contact therewith. The EAM category includes molecules used in MALDI, frequently referred to as "matrix," and is exemplified by cinnamic acid derivatives, sinapinic acid (SPA), cyano-hydroxy-cinnamic acid (CHCA) and dihydroxybenzoic acid, ferulic acid, and hydroxyaceto-phenone derivatives. The category also includes EAMs used in SELDI, as enumerated, for example, by U.S. 5,719,060 and U.S. 60/351,971 (Kitagawa), filed January 25, 2002. [0073] Another version of SELDI, called Surface-Enhanced Photolabile Attachment and Release (SEPAR), involves the use of probes having moieties attached to the surface that can covalently bind an analyte, and then release the analyte through breaking a photolabile bond in the moiety after exposure to light, e.g., to laser light.

For instance, see U.S. 5,719,060. SEPAR and other forms of SELDI are readily adapted to detecting a biomarker or biomarker profile, pursuant to the present invention.

[0074] The detection of the biomarkers according to the invention can be enhanced by using certain selectivity conditions, e.g., adsorbents or washing solutions. The phrase "wash solution" refers to an agent, typically a solution, which is used to affect or modify adsorption of an analyte to an adsorbent surface and/or to remove unbound materials from the surface. The elution characteristics of a wash solution can depend, for example, on pH, ionic strength, hydrophobicity, degree of chaotropism, detergent strength, and temperature.

[0075] Pursuant to one aspect of the present invention, a sample is analyzed by means of a "biochip," a term that denotes a solid substrate, having a generally planar surface, to which a capture reagent (adsorbent) is attached. Frequently, the surface of a biochip comprises a plurality of addressable locations, each of which has the capture reagent bound there. A biochip can be adapted to engage a probe interface and, hence, function as a probe in gas phase ion spectrometry preferably mass spectrometry. Alternatively, a biochip of the invention can be mounted onto another substrate to form a probe that can be inserted into the spectrometer.

[0076] A variety of biochips is available for the capture of biomarkers, in accordance with the present invention, from commercial sources such as Ciphergen Biosystems (Fremont, CA), Perkin Elmer (Packard BioScience Company (Meriden CT), Zyomyx (Hayward, CA), and Phylos (Lexington, MA). Exemplary of these biochips are those described in U.S. patents No. 6,225,047, supra, and No. 6,329,209 (Wagner et al.), and in PCT publications WO 99/51773 (Kuimelis and Wagner) and WO 00/56934 (Englert et al.).

[0077] More specifically, biochips produced by Ciphergen Biosystems have surfaces, presented on an aluminum substrate in strip form, to which are attached, at addressable locations, chromatographic or biospecific adsorbents. The surface of the strip is coated with silicon dioxide.

[0078] Illustrative of Ciphergen ProteinChip® arrays are biochips H4, SAX-2, WCX-2, and IMAC-3, which include a functionalized, cross-linked polymer in the

form of a hydrogel, physically attached to the surface of the biochip or covalently attached through a silane to the surface of the biochip. The H4 biochip has isopropyl functionalities for hydrophobic binding. The SAX-2 biochip has quaternary ammonium functionalities for anion exchange. The WCX-2 biochip has carboxylate functionalities for cation exchange. The IMAC-3 biochip has nitriloacetic acid functionalities that adsorb transition metal ions, such as Cu++ and Ni++, by chelation. These immobilized metal ions, in turn, allow for adsorption of biomarkers by coordinate covalent bonding. Thus, Ciphergen's IMAC ProteinChip® arrays are sold with reactive moieties that become adsorbent upon the addition by the user of a metal solution.

[0079] In keeping with the above-described principles, a substrate with an adsorbent is contacted with the sample, containing serum, for a period of time sufficient to allow biomarker that may be present to bind to the adsorbent. In one embodiment of the invention, more than one type of substrate with adsorbent thereon is contacted with the biological sample. For example, a sample may be applied to both a WCX and an IMAC chip. This technique can allow for even more definitive assessment of cancer status. After the incubation period, the substrate is washed to remove unbound material. Any suitable washing solutions can be used; preferably, aqueous solutions are employed.

[0080] An energy absorbing molecule then is applied to the substrate with the bound biomarkers. As noted, an energy absorbing molecule is a molecule that absorbs energy from an energy source such as a laser, thereby assisting in desorption of biomarkers from the substrate. Exemplary energy absorbing molecules include, as noted above, cinnamic acid derivatives, sinapinic acid and dihydroxybenzoic acid. Preferably sinapinic acid is used.

[0081] The biomarkers bound to the substrates are detected in a gas phase ion spectrometer such as a time-of-flight mass spectrometer. The biomarkers are ionized by an ionization source such as a laser, the generated ions are collected by an ion optic assembly, and then a mass analyzer disperses and analyzes the passing ions. The detector then translates information of the detected ions into mass-to-charge

ratios. Detection of a biomarker typically will involve detection of signal intensity. Thus, both the quantity and mass of the biomarker can be determined.

[0082] Data generated by desorption and detection of biomarkers can be analyzed

with the use of a programmable digital computer. The computer program analyzes the data to indicate the number of markers detected, and optionally the strength of the signal and the determined molecular mass for each biomarker detected. Data analysis can include steps of determining signal strength of a biomarker and removing data deviating from a predetermined statistical distribution. For example, the observed peaks can be normalized, by calculating the height of each peak relative to some reference. The reference can be background noise generated by the instrument and chemicals such as the energy absorbing molecule which is set as zero in the scale. [0083] The computer can transform the resulting data into various formats for display. The standard spectrum can be displayed, but in one useful format only the peak height and mass information are retained from the spectrum view, yielding a cleaner image and enabling biomarkers with nearly identical molecular weights to be more easily seen. In another useful format, two or more spectra are compared, conveniently highlighting unique biomarkers and biomarkers that are up- or downregulated between samples. Using any of these formats, one can readily determine whether a particular biomarker is present in a sample.

[0084] Software used to analyze the data can include code that applies an algorithm to the analysis of the signal to determine whether the signal represents a peak in a signal that corresponds to a biomarker according to the present invention. The software also can subject the data regarding observed biomarker peaks to classification tree or ANN analysis, to determine whether a biomarker peak or combination of biomarker peaks is present that indicates lung cancer status. Analysis of the data may be "keyed" to a variety of parameters that are obtained either directly or indirectly from the mass spectrometric analysis of the sample. These parameters include, but are not limited to, the presence or absence of one or more peaks, the height of one or more peaks, the log of the height of one or more peaks, and other arithmetic manipulations of peak height data.

[0085] In another aspect, the present invention provides kits for aiding in the diagnosis of lung cancer status, which kits are used to detect biomarkers according to the invention. The kits screen for the presence of biomarkers and combinations of biomarkers that are differentially present in samples from normal subjects and subjects with lung cancer.

[0086] In one embodiment, the kit comprises a substrate having an adsorbent thereon, wherein the adsorbent is suitable for binding a biomarker according to the invention, and a washing solution or instructions for making a washing solution, in which the combination of the adsorbent and the washing solution allows detection of the biomarker using gas phase ion spectrometry, e.g., mass spectrometry. The kit may include more than type of adsorbent, each present on a different substrate.

[0087] In another embodiment, a kit of the invention may include a first substrate, comprising an adsorbent thereon, and a second substrate onto which the first substrate is positioned to form a probe, which can be inserted into a gas phase ion spectrometer, e.g., a mass spectrometer. In another embodiment, an inventive kit may comprise a single substrate that can be inserted into the spectrometer.

[0088] In a further embodiment, such a kit can comprise instructions for suitable operational parameters in the form of a label or separate insert. For example, the instructions may inform a consumer how to collect the sample or how to wash the probe. In yet another embodiment the kit can comprise one or more containers with biomarker samples, to be used as standard(s) for calibration.

[0089] In a preferred embodiment, the detection of biomarkers for diagnosis of lung cancer in a subject entails contacting a sample from a subject or patient, preferably a serum sample, with a substrate having an adsorbent thereon under conditions that allow binding between the biomarker and the adsorbent, and then detecting the biomarker bound to the adsorbent by gas phase ion spectrometry, preferably by Surface Enhanced Laser Desorption/Ionization (SELDI) mass spectrometry. The biomarkers are ionized by an ionization source such as a laser. The generated ions are collected by an ion optic assembly and accelerated toward an ion detector. Ions that strike the detector generate an electric potential that is digitized by a high speed time-array recording device that digitally captures the analog signal. Ciphergen's

ProteinChip® system employs an analog-to-digital converter (ADC) to accomplish this. The ADC integrates detector output at regularly spaced time intervals into time-dependent bins. The time intervals typically are one to four nanoseconds long. Furthermore, the time-of-flight spectrum ultimately analyzed typically does not represent the signal from a single pulse of ionizing energy against a sample, but rather the sum of signals from a number of pulses. This reduces noise and increases dynamic range. This time-of-flight data is then subject to data processing. In Ciphergen's ProteinChip® software, data processing typically includes TOF-to-M/Z transformation, baseline subtraction, high frequency noise filtering. Thus, both the quantity and mass of the biomarker can be determined.

[0090] The detection of the biomarkers can be enhanced by using certain selectivity conditions, e.g., adsorbents or washing solutions. In one embodiment, the same or similar selectivity conditions that were used to discover the biomarkers are used in the method of detecting the biomarker in the sample. For example, immobilized metal affinity capture chips such as the Cu(II) IMAC3 and weak cationic exchange chips such as the WCX2 chips are preferred as the adsorbents for biomarker detection. However, other adsorbents can be used, as long as they have the binding characteristics suitable for binding the biomarkers.

[0091] More particularly, armed with the information regarding the biomarkers identified herein, various methods can be used to recognize patterns of doublets, triplets, and higher combinations of biomarkers according to the invention. These methods take raw data regarding which peaks are present and their intensity and provide a differential diagnosis of lung cancer versus normal for a sample.

[0092] Thus, the process can be divided into the learning phase and the classification phase. In the learning phase, a learning algorithm is applied to a data set that includes members of the different classes that are meant to be classified, for example, data from a plurality of samples diagnosed as cancer and data from a plurality of samples assigned a negative diagnosis. The methods used to analyze the data include, but are not limited to, artificial neural network, support vector machines, genetic algorithm and self-organizing maps and classification and regression tree analysis. These methods are described, for example, in WO 01/31579, May 3, 2001

(Barnhill et al.); WO 02/06829, January 24, 2002 (Hitt et al.) and WO 02/42733, May 30, 2002 (Paulse et al.). The learning algorithm produces a classifying algorithm. The classifier is keyed to elements of the data, such as particular markers and particular intensities of markers, usually in combination, that can classify an unknown sample into one of the two classes. The classifier is ultimately used for diagnostic testing.

[0093] Software, both freeware and proprietary software, is readily available to analyze such patterns in data, and to devise additional patterns with any predetermined criteria for success. Those biomarkers which by themselves are predictive of a differential diagnosis of lung cancer versus normal do not require pattern recognition software to analyze the data.

[0094] The following examples are offered by way of illustration, and are not limiting.

Example I. Fractionation of serum

Buffers:

- 1. U9 (9M urea, 2% CHAPS, 50mM Tris-HCl pH9)
- 2. U1 (1M urea, 0.22% CHAPS, 50mM Tris-HCl pH9)
- 3. wash buffer 1: 50mM Tris-HCl with 0.1% n-octyl I-D-Glucopyranoside (OGP) pH9
- 4. wash buffer 2: 100mM sodium phosphate with 0.1% OGP pH7
- 5. wash buffer 3: 100mM sodium acetate with 0.1% OGP pH5
- 6. wash buffer 4: 100mM sodium acetate with 0.1% OGP pH4
- 7. wash buffer 5: 50mM sodium citrate with 0.1% OGP pH3
- 8. wash buffer 6: 33.3% isopropanol / 16.7% acetonitrile / 0.1% trifluoroacetic acid in water.

[0095] Thirty microliters of U9 buffer were added to 20µL of serum in a tube and were mixed at 4°C for 20 minutes. Ion exchange resin (Q Ceramic HyperDF ion exchange resin, Biosepra SA, France) was washed 3 times with 5 bed volumes of 50mM Tris-HCl pH9 and stored in 50% suspension. To each well of a 96-well filter plate (96-well Silent Screen filter plate. Loprodyne membrane, 0.45 micron pore,

Nalge Nunc International, USA), 125 µL of ion exchange resin (50% suspension) was added on a Biomek 2000 Automation Workstation (Beckman Coulter, Fullerton, CA), washed 3 times with 150µL U1 buffer, and vacuum dried. Urea-treated serum was transferred to each well of ion exchange resin. The serum tube was rinsed with 50µL of U1 buffer, which was also transferred to the corresponding well in filter plate. The filter plate was mixed on a platform shaker at 4°C for 30 minutes. Flow-through fraction was collected in a 96-well plate by vacuum suction (Fraction 1). Then, 100µL of wash buffer 1 was added to each well of filter plate and mixed for 10 minutes at room temperature. Eluant was collected into the same 96-well plate (Fraction 1). Resins in the filter plate were subsequently washed two times each with 100µL wash buffers 2, 3, 4, 5 and 6. Each eluant (total volume of 200µL) was collected in a 96-well plate (Fractions 2,3,4,5 and 6).

Example 2. SELDI analysis of fractionated serum

[0096] ProteinChip® Arrays were set up in 96-well bioprocessors. Buffer delivery and sample incubation were performed on a Biomek 2000 Automation Workstation. Each serum fraction was analyzed on IMAC3 (loaded with copper) and WCX2 ProteinChip® Arrays in duplicates. IMAC3 copper and WCX2 arrays (Ciphergen Biosystems Inc, Fremont, CA) were equilibrated two times with 150μL of binding buffer (100mM sodium phosphate + 0.5M NaCl pH7 for IMAC3, 100mM sodium acetate pH4 for WCX2). Each serum fraction was diluted in the corresponding binding buffer (1/5 dilution for IMAC3 and 1/10 dilution for WCX2) and 100μL was applied to each ProteinChip® array. Incubation was performed on a platform shaker at room temperature for 30 minutes. Each array was washed three times with 150μL of corresponding binding buffer and rinsed two times with water. ProteinChip® arrays were air-dried. Sinapinic acid matrix (prepared in 50% acetonitrile, 0.5% trifluoroacetic acid) was applied to each array. ProteinChip® arrays were read on a ProteinChip® PBSII Reader (Ciphergen Biosystems Inc.) A total of 253 laser shots were averaged for each array.

[0097] All publications and patent documents cited in this application are incorporated by reference in their entirety for all purposes to the same extent as if

each individual publication or patent document were so individually denoted. By their citation of various references in this document Applicants do not admit that any particular reference is "prior art" to their invention.

What we claim is:

- 1. A method for qualifying lung carcinoma status in a subject, comprised of analyzing a biological sample from said subject for a diagnostic level of a protein selected from either a first group consisting of
- (i) IM-522, IM-273, IM-520, IM-519, IM-454, IM-507, IM-521, IM-148, IM-266, IM-537, IM-471, IM-510, IM-544, IM-474, IM-155, IM-157, IM-176, IM-445, IM-177, IM-440, IM-468, IM-438, IM-547, IM-359, IM-436, IM-106, IM-455, IM-444, IM-158, IM-265, IM-50, IM-159, IM-156, IM-439, IM-157, IM-508, IM-514, IM-478, IM-473, IM-360, IM-435, IM-150, IM-151, IM-110, IM-51, IM-163, IM-437, IM-546, IM-153, and IM-268,

or from a second group consisting of

(ii) WM-61, WM-447, WM-446, WM-133, WM-119, WM-278, WM-134, WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, WM-70, WM-369, WM-17, WM-473, WM-47, WM-203, WM-276, WM-279, WM-62, WM-366, WM-456, WM-428, WM-384, WM-287, WM-420, WM-292, WM-431, WM-455, WM-20, WM-340, WM-105, WM-389, WM-63, WM-354, WM-450, WM-466, WM-296, WM-343, WM-341, WM-339, WM-55, WM-66, WM-48, WM-38, WM-138, and WM-310,

wherein the biomarker is differentially present in samples of a subject with lung cancer and a normal subject that is free of lung cancer.

- 2. The method according to claim 1, wherein the protein is selected from either a first group consisting of
- (i) IM-522, IM-273, IM-520, IM-519, IM-454, IM-507, IM-521, IM-148, IM-266, IM-537, IM-471, IM-510, IM-544, IM-474, and IM-155,

or from a second group consisting of

- (ii) WM-61, WM-447, WM-446, WM-133, WM-119, WM-278, WM-134, WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, and WM-70.
- 3. The method according to claim 1, wherein the protein is selected from either a first group consisting of
 - (i) IM-522, IM-273, IM-520, IM-519, and IM-454, or from a second group consisting

- (ii) WM-61, WM-447, WM-446, WM-133, and WM-119.
- 4. The method according to claim 1, which uses a single biomarker selected from the group consisting of the WM-446 and WM-447.
 - 5. A method for qualifying lung carcinoma risk in a subject, comprising
- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- (B) extracting data from the spectrum and subjecting the data to patternrecognition analysis that is keyed to at least one peak selected from either a first group consisting of
- (i) IM-522, IM-273, IM-520, IM-519, IM-454, IM-507, IM-521, IM-148, IM-266, IM-537, IM-471, IM-510, IM-544, IM-474, IM-155, IM-157, IM-176, IM-445, IM-177, IM-440, IM-468, IM-438, IM-547, IM-359, IM-436, IM-106, IM-455, IM-444, IM-158, IM-265, IM-50, IM-159, IM-156, IM-439, IM-157, IM-508, IM-514, IM-478, IM-473, IM-360, IM-435, IM-150, IM-151, IM-110, IM-51, IM-163, IM-437, IM-546, IM-153, and IM-268,

or from a second group consisting of

- (ii) WM-61, WM-447, WM-446, WM-133, WM-119, WM-278, WM-134, WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, WM-70, WM-369, WM-17, WM-473, WM-47, WM-203, WM-276, WM-279, WM-62, WM-366, WM-456, WM-428, WM-384, WM-287, WM-420, WM-292, WM-431, WM-455, WM-20, WM-340, WM-105, WM-389, WM-63, WM-354, WM-450, WM-466, WM-296, WM-343, WM-341, WM-339, WM-55, WM-66, WM-48, WM-38, WM-138, and WM-310.
- 6. The method according to claim 5, wherein the pattern-recognition analysis is keyed to a pair of peaks selected either from a first group consisting of
- (i) IM-266 and IM-474, IM-266 and IM-38, IM-266 and IM-454, IM-266 and IM-522, IM- 266 and IM-544, IM-266 and IM-471, IM-474 and IM-151, IM-474 and IM-156, IM-474 and IM-544, IM-474 and IM-38, IM-522 and IM-507, IM-522 and IM-156, and IM-522 and IM-440;

or from a second group consisting of

- (ii) WM-447 and WM-59, WM-447 and WM-19, WM-447 and WM-118, WM-447 and WM-473, WM-19 and WM-59, WM-19 and WM-473, WM-19 and WM-369, WM-61 and WM-154, WM-61 and WM-369, WM-118 and WM-59 and WM-282 and WM-127.
- 7. The method according to claim 5, wherein the pattern-recognition analysis is keyed to a pair of peaks selected from either a first group consisting of
 - (i) IM-266 and IM-474, IM-266 and IM-544, and IM-156 and IM-522; or from a second group consisting of
 - (ii) WM-447 and WM-59, WM-447 and WM-19, and WM-19 and WM-59.
- 8. The method according to claim 5, wherein the pattern-recognition analysis is keyed to a triplet of peaks selected from
 - (i) IM-266, IM-454 and IM-474; and IM-266, IM-474 and IM-544; or wherein the analysis is keyed to
 - (ii) WM-447, WM-19 and WM-473.
 - 9. A kit for detecting and diagnosing lung carcinoma, comprising
- (A) an adsorbent attached to a substrate that retains one or more of the biomarkers selected from either a first group consisting of
- (i) IM-522, IM-273, IM-520, IM-519, IM-454, IM-507, IM-521, IM-148, IM-266, IM-537, IM-471, IM-510, IM-544, IM-474, IM-155, IM-157, IM-176, IM-445, IM-177, IM-440, IM-468, IM-438, IM-547, IM-359, IM-436, IM-106, IM-455, IM-444, IM-158, IM-265, IM-50, IM-159, IM-156, IM-439, IM-157, IM-508, IM-514, IM-478, IM-473, IM-360, IM-435, IM-150, IM-151, IM-110, IM-51, IM-163, IM-437, IM-546, IM-153, and IM-268,

or from a second group consisting of

(ii) WM-61, WM-447, WM-446, WM-133, WM-119, WM-278, WM-134, WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, WM-70, WM-369, WM-17, WM-473, WM-47, WM-203, WM-276, WM-279, WM-62, WM-366, WM-456, WM-428, WM-384, WM-287, WM-420, WM-292, WM-431, WM-455, WM-20, WM-340, WM-105, WM-389, WM-63, WM-354, WM-450, WM-466, WM-296, WM-343, WM-341, WM-339, WM-55, WM-66, WM-48, WM-38, WM-138, and WM-310, and

- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- 10. A kit according to claim 9, further comprising a washing solution or instructions for making a washing solution.
- 11. A kit according to claim 9, wherein the substrate is a SELDI probe that comprises either (i) functionalities that adsorb transition metal ions by chelation or (ii) functionalities that allow for cation exchange.
- 12. A method for qualifying lung adenocarcinoma status in a subject, comprised of analyzing a biological sample from said subject for a level of a protein selected from the group consisting of WM-447, WM-652, WM-61, WM-446, WM-290, WM-363, WM-133, WM-341, WM-285, WM-366, WM-282, WM-362, WM-310, WM-292, WM-120, WM-134, WM-276, WM-428, WM-277, WM-20, WM-119, WM-340, WM-48, WM-389, WM-450, WM-47, WM-343, WM-17, WM-583, WM-70, WM-706, WM-346, WM-466, WM-646, WM-384, WM-336, WM-294, WM-339, WM-473, WM-369, WM-38, WM-283, WM-685, WM-66, WM-55, WM-650, WM-307, WM-278, WM-342, and WM-429.
- 13. The method according to claim 12, wherein the protein is selected from the group consisting of WM-447, WM-652, WM-61, WM-446, WM-290, WM-363, WM-133, WM-341, WM-285, WM-366, WM-282, WM-362, WM-310, WM-292, and WM-120.
- 14. The method according to claim 12, wherein the protein is selected from the group consisting of WM-447, WM-652, WM-61, WM-446, WM-290.
- 15. A method for qualifying status of lung adenocarcinoma in a subject, comprising
- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- (B) extracting data from the spectrum and subjecting the data to pattern-recognition analysis that is keyed to at least one peak selected from either a first group consisting of WM-447, WM-652, WM-61, WM-446, WM-290, WM-363, WM-133, WM-341, WM-285, WM-366, WM-282, WM-362, WM-310, WM-292, WM-120, WM-134, WM-276, WM-428, WM-277, WM-20, WM-119, WM-340, WM-48, WM-

389, WM-450, WM-47, WM-343, WM-17, WM-583, WM-70, WM-706, WM-346, WM-466, WM-646, WM-384, WM-336, WM-294, WM-339, WM-473, WM-369, WM-38, WM-283, WM-685, WM-66, WM-55, WM-650, WM-307, WM-278, WM-342, and WM-429.

- 16. The method according to claim 15, wherein the protein is selected from the group consisting of WM-447, WM-652, WM-61, WM-446, WM-290, WM-363, WM-133, WM-341, WM-285, WM-366, WM-282, WM-362, WM-310, WM-292, and WM-120.
- 17. The method according to claim 15, wherein the protein is selected from the group consisting of WM-447, WM-652, WM-61, WM-446, WM-290.
 - 18. A kit for detecting and diagnosing lung adenocarcinoma, comprising
- (A) an adsorbent attached to a substrate that retains one or more of biomarkers selected from the group consisting of WM-447, WM-652, WM-61, WM-446, WM-290, WM-363, WM-133, WM-341, WM-285, WM-366, WM-282, WM-362, WM-310, WM-292, WM-120, WM-134, WM-276, WM-428, WM-277, WM-20, WM-119, WM-340, WM-48, WM-389, WM-450, WM-47, WM-343, WM-17, WM-583, WM-70, WM-706, WM-346, WM-466, WM-646, WM-384, WM-336, WM-294, WM-339, WM-473, WM-369, WM-38, WM-283, WM-685, WM-66, WM-55, WM-650, WM-307, WM-278, WM-342, and WM-429, and
- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- 19. A kit according to claim 18, further comprising a washing solution or instructions for making a washing solution.
- 20. A kit according to claim 18, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.
- 21. A method for qualifying squamous cell lung carcinoma status in a subject, comprised of analyzing a biological sample from said subject for a level of a protein selected from the group consisting of WM-447, WM-61, WM-277, WM-446, WM-133, WM-134, WM-363, WM-362, WM-276, WM-706, WM-203, WM-466, WM-366, WM-65, WM-70, WM-341, WM-429, WM-347, WM-17, WM-47, WM-431, WM-62, WM-473, WM-384, WM-438, WM-652, WM-282, WM-389, WM-290,

WM-278, WM-456, WM-673, WM-340, WM-55, WM-455, WM-645, WM-138, WM-420, WM-450, WM-369, WM-279, WM-342, WM-471, WM-674, WM-120, WM-20, WM-287, WM-83, WM-154, and WM-128.

- 22. The method according to claim 21, wherein the protein is selected from the group consisting of WM-447, WM-61, WM-277, WM-446, WM-133, WM-134, WM-363, WM-362, WM-276, WM-706, WM-203, WM-466, WM-366, WM-65, and WM-70.
- 23. The method according to claim 21, wherein the protein is selected from the group consisting of WM-447, WM-61, WM-277, WM-446, and WM-133.
- 24. A method for qualifying status of squamous cell lung carcinoma in a subject, comprising
- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- (B) extracting data from the spectrum and subjecting the data to pattern-recognition analysis that is keyed to at least one peak selected from either a first group consisting of WM-447, WM-61, WM-277, WM-446, WM-133, WM-134, WM-363, WM-362, WM-276, WM-706, WM-203, WM-466, WM-366, WM-65, WM-70, WM-341, WM-429, WM-347, WM-17, WM-47, WM-431, WM-62, WM-473, WM-384, WM-438, WM-652, WM-282, WM-389, WM-290, WM-278, WM-456, WM-673, WM-340, WM-55, WM-455, WM-645, WM-138, WM-420, WM-450, WM-369, WM-279, WM-342, WM-471, WM-674, WM-120, WM-20, WM-287, WM-83, WM-154, and WM-128.
- 25. The method according to claim 24, wherein the protein is selected from the group consisting of WM-447, WM-61, WM-277, WM-446, WM-133, WM-134, WM-363, WM-362, WM-276, WM-706, WM-203, WM-466, WM-366, WM-65, and WM-70.
- 26. The method according to claim 24, wherein the protein is selected from the group consisting of WM-447, WM-61, WM-277, WM-446, and WM-133.
- A kit for detecting and diagnosing squamous cell lung carcinoma,
 comprising

- (A) an adsorbent attached to a substrate that retains one or more of the biomarkers selected from the group consisting of WM-447, WM-61, WM-277, WM-446, WM-133, WM-134, WM-363, WM-362, WM-276, WM-706, WM-203, WM-466, WM-366, WM-65, WM-70, WM-341, WM-429, WM-347, WM-17, WM-47, WM-431, WM-62, WM-473, WM-384, WM-438, WM-652, WM-282, WM-389, WM-290, WM-278, WM-456, WM-673, WM-340, WM-55, WM-455, WM-645, WM-138, WM-420, WM-450, WM-369, WM-279, WM-342, WM-471, WM-674, WM-120, WM-20, WM-287, WM-83, WM-154, and WM-128, and
- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- 28. A kit according to claim 27, further comprising a washing solution or instructions for making a washing solution.
- 29. A kit according to claim 27, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.
- 30. A method for qualifying small cell lung carcinoma status in a subject, comprised of analyzing a biological sample from said subject for a level of a protein selected from the group consisting of WM-70, WM-706, WM-369, WM-447, WM-61, WM-652, WM-282, WM-446, WM-456, WM-134, WM-203, WM-646, WM-455, WM-65, WM-685, WM-473, WM-343, WM-466, WM-341, WM-340, WM-363, WM-339, WM-457, WM-86, WM-506, WM-72, WM-287, WM-82, WM-528, WM-85, WM-73, WM-138, WM-384, WM-83, WM-450, WM-310, WM-277, WM-79, WM-207, WM-278, WM-290, WM-366, WM-472, WM-420, WM-147, WM-55, WM-669, WM-357, WM-429, and WM-279.
- 31. The method according to claim 30, wherein the protein is selected from the group consisting of WM-70, WM-706, WM-369, WM-447, WM-61, WM-652, WM-282, WM-446, WM-456, WM-134, WM-203, WM-646, WM-455, WM-65, and WM-685.
- 32. The method according to claim 30, wherein the protein is selected from the group consisting of WM-70, WM-706, WM-369, WM-447, and WM-61.
- 33. A method for qualifying status of small cell lung carcinoma in a subject, comprising

- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- (B) extracting data from the spectrum and subjecting the data to pattern-recognition analysis that is keyed to at least one peak selected from either a first group consisting of WM-70, WM-706, WM-369, WM-447, WM-61, WM-652, WM-282, WM-446, WM-456, WM-134, WM-203, WM-646, WM-455, WM-65, WM-685, WM-473, WM-343, WM-466, WM-341, WM-340, WM-363, WM-339, WM-457, WM-86, WM-506, WM-72, WM-287, WM-82, WM-528, WM-85, WM-73, WM-138, WM-384, WM-83, WM-450, WM-310, WM-277, WM-79, WM-207, WM-278, WM-290, WM-366, WM-472, WM-420, WM-147, WM-55, WM-669, WM-357, WM-429, and WM-279.
- 34. The method according to claim 33, wherein the protein is selected from the group consisting of WM-70, WM-706, WM-369, WM-447, WM-61, WM-652, WM-282, WM-446, WM-456, WM-134, WM-203, WM-646, WM-455, WM-65, and WM-685.
- 35. The method according to claim 33, wherein the protein is selected from the group consisting of WM-70, WM-706, WM-369, WM-447, and WM-61.
- 36. A kit for detecting and diagnosing small cell lung carcinoma, comprising
- (A) an adsorbent attached to a substrate that retains one or more of the biomarkers selected from the group consisting of WM-70, WM-706, WM-369, WM-447, WM-61, WM-652, WM-282, WM-446, WM-456, WM-134, WM-203, WM-646, WM-455, WM-65, WM-685, WM-473, WM-343, WM-466, WM-341, WM-340, WM-363, WM-339, WM-457, WM-86, WM-506, WM-72, WM-287, WM-82, WM-528, WM-85, WM-73, WM-138, WM-384, WM-83, WM-450, WM-310, WM-277, WM-79, WM-207, WM-278, WM-290, WM-366, WM-472, WM-420, WM-147, WM-55, WM-669, WM-357, WM-429, and WM-279, and
- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- 37. A kit according to claim 36, further comprising a washing solution or instructions for making a washing solution.

- 38. A kit according to claim 36, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.
- 39. A method for qualifying non-small cell lung carcinoma status in a subject, comprised of analyzing a biological sample from said subject for a level of a protein selected from the group consisting of WM-341, WM-342, WM-343, WM-48, WM-340, WM-346, WM-47, WM-339, WM-389, WM-669, WM-447, WM-652, WM-154, WM-587, WM-456, WM-450, WM-283, WM-207, WM-436, WM-384, WM-61, WM-167, WM-382, WM-285, WM-650, WM-203, WM-119, WM-282, WM-686, WM-383, WM-429, WM-11, WM-208, WM-451, WM-473, WM-220, WM-685, WM-338, WM-71, WM-266, WM-70, WM-545, WM-675, WM-446, WM-120, WM-267, WM-466, WM-347, WM-153, and WM-38.
- 40. The method according to claim 39, wherein the protein is selected from the group consisting of WM-341, WM-342, WM-343, WM-48, WM-340, WM-346, WM-47, WM-339, WM-389, WM-669, WM-447, WM-652, WM-154, WM-587, and WM-456.
- 41. The method according to claim 39, wherein the protein is selected from the group consisting of WM-341, WM-342, WM-343, WM-48, and WM-340.
- 42. A method for qualifying status of non-small cell lung carcinoma in a subject, comprising
- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- (B) extracting data from the spectrum and subjecting the data to pattern-recognition analysis that is keyed to at least one peak selected from the group consisting of WM-341, WM-342, WM-343, WM-48, WM-340, WM-346, WM-47, WM-339, WM-389, WM-669, WM-447, WM-652, WM-154, WM-587, WM-456, WM-450, WM-283, WM-207, WM-436, WM-384, WM-61, WM-167, WM-382, WM-285, WM-650, WM-203, WM-119, WM-282, WM-686, WM-383, WM-429, WM-11, WM-208, WM-451, WM-473, WM-220, WM-685, WM-338, WM-71, WM-266, WM-70, WM-545, WM-675, WM-446, WM-120, WM-267, WM-466, WM-347, WM-153, and WM-38.

- 43. The method according to claim 42, wherein the protein is selected from the group consisting of WM-341, WM-342, WM-343, WM-48, WM-340, WM-346, WM-47, WM-339, WM-389, WM-669, WM-447, WM-652, WM-154, WM-587, and WM-456.
- 44. The method according to claim 42, wherein the protein is selected from the group consisting of WM-341, WM-342, WM-343, WM-48, and WM-340.
- 45. A kit for detecting and diagnosing non-small cell lung carcinoma, comprising
- (A) an adsorbent attached to a substrate that retains one or more of the biomarkers WM-341, WM-342, WM-343, WM-48, WM-340, WM-346, WM-47, WM-339, WM-389, WM-669, WM-447, WM-652, WM-154, WM-587, WM-456, WM-450, WM-283, WM-207, WM-436, WM-384, WM-61, WM-167, WM-382, WM-285, WM-650, WM-203, WM-119, WM-282, WM-686, WM-383, WM-429, WM-11, WM-208, WM-451, WM-473, WM-220, WM-685, WM-338, WM-71, WM-266, WM-70, WM-545, WM-675, WM-446, WM-120, WM-267, WM-466, WM-347, WM-153, and WM-38, and
- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- 46. A kit according to claim 45, further comprising a washing solution or instructions for making a washing solution.
- 47. A kit according to claim 45, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.
- 48. A method for qualifying large cell lung carcinoma status in a subject, comprised of analyzing a biological sample from said subject for a level of a protein selected from the group consisting of WM-16, WM-26, WM-499, WM-134, WM-647, WM-277, WM-310, WM-363, WM-446, WM-221, WM-648, WM-657, WM-290, WM-328, WM-447, WM-684, WM-183, WM-190, WM-686, WM-397, WM-466, WM-20, WM-17, WM-545, WM-47, WM-191, WM-147, WM-480, WM-590, WM-218, WM-285, WM-652, WM-651, WM-366, WM-403, WM-418, WM-430, WM-456, WM-714, WM-646, WM-109, WM-302, WM-587, WM-375, WM-131, WM-706, WM-398, WM-309, WM-55, and WM-488.

- 49. The method according to claim 48, wherein the protein is selected from the group consisting of WM-16, WM-26, WM-499, WM-134, WM-647, WM-277, WM-310, WM-363, WM-446, WM-221, WM-648, WM-657, WM-290, WM-328, and WM-447.
- 50. The method according to claim 48, wherein the protein is selected from the group consisting of WM-16, WM-26, WM-499, WM-134, and WM-647.
- 51. A method for qualifying status of large cell lung carcinoma in a subject, comprising
- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- (B) extracting data from the spectrum and subjecting the data to pattern-recognition analysis that is keyed to at least one peak selected from the group consisting of WM-16, WM-26, WM-499, WM-134, WM-647, WM-277, WM-310, WM-363, WM-446, WM-221, WM-648, WM-657, WM-290, WM-328, WM-447, WM-684, WM-183, WM-190, WM-686, WM-397, WM-466, WM-20, WM-17, WM-545, WM-47, WM-191, WM-147, WM-480, WM-590, WM-218, WM-285, WM-652, WM-651, WM-366, WM-403, WM-418, WM-430, WM-456, WM-714, WM-646, WM-109, WM-302, WM-587, WM-375, WM-131, WM-706, WM-398, WM-309, WM-55, and WM-488.
- 52. The method according to claim 51, wherein the protein is selected from the group consisting of WM-16, WM-26, WM-499, WM-134, WM-647, WM-277, WM-310, WM-363, WM-446, WM-221, WM-648, WM-657, WM-290, WM-328, and WM-447.
- 53. The method according to claim 51, wherein the protein is selected from the group consisting of WM-16, WM-26, WM-499, WM-134, and WM-647.
- 54. A kit for detecting and diagnosing large cell lung carcinoma, comprising
- (A) an adsorbent attached to a substrate that retains one or more of the biomarkers WM-16, WM-26, WM-499, WM-134, WM-647, WM-277, WM-310, WM-363, WM-446, WM-221, WM-648, WM-657, WM-290, WM-328, WM-447, WM-684, WM-183, WM-190, WM-686, WM-397, WM-466, WM-20, WM-17, WM-

545, WM-47, WM-191, WM-147, WM-480, WM-590, WM-218, WM-285, WM-652, WM-651, WM-366, WM-403, WM-418, WM-430, WM-456, WM-714, WM-646, WM-109, WM-302, WM-587, WM-375, WM-131, WM-706, WM-398, WM-309, WM-55, and WM-488, and

- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- 55. A kit according to claim 50, further comprising a washing solution or instructions for making a washing solution.
- 56. A kit according to claim 50, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.
- 57. A method for distinguishing lung adenocarcinoma from squamous lung carcinoma in a subject, comprised of analyzing a biological sample from said subject for a level of a protein selected from the group consisting of WM-62, WM-415, WM-152, WM-385, WM-347, WM-134, WM-36, WM-108, WM-99, WM-151, WM-289, WM-363, WM-61, WM-117, WM-211, WM-362, WM-133, WM-414, WM-277, WM-141, WM-64, WM-135, WM-447, WM-383, WM-338, WM-63, WM-142, WM-446, WM-186, WM-111, WM-445, WM-455, WM-276, WM-444, WM-181, WM-35, WM-285, WM-456, WM-39, WM-82, WM-17, WM-203, WM-83, WM-412, WM-96, WM-74, WM-457, WM-431, WM-340, and WM-49.
- 58. The method according to claim 57, wherein the protein is selected from the group consisting of WM-62, WM-415, WM-152, WM-385, WM-347, WM-134, WM-36, WM-108, WM-99, WM-151, WM-289, WM-363, WM-61, WM-117, and WM-211.
- 59. The method according to claim 57, wherein the protein is selected from the group consisting of WM-62, WM-415, WM-152, WM-385, and WM-347.
- 60. A method for distinguishing lung adenocarcinoma from squamous lung carcinoma in a subject, comprising
- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- (B) extracting data from the spectrum and subjecting the data to patternrecognition analysis that is keyed to at least one peak selected from the group

consisting of WM-62, WM-415, WM-152, WM-385, WM-347, WM-134, WM-36, WM-108, WM-99, WM-151, WM-289, WM-363, WM-61, WM-117, WM-211, WM-362, WM-133, WM-414, WM-277, WM-141, WM-64, WM-135, WM-447, WM-383, WM-338, WM-63, WM-142, WM-446, WM-186, WM-111, WM-445, WM-455, WM-276, WM-444, WM-181, WM-35, WM-285, WM-456, WM-39, WM-82, WM-17, WM-203, WM-83, WM-412, WM-96, WM-74, WM-457, WM-431, WM-340, and WM-49.

- 61. The method according to claim 60, wherein the protein is selected from the group consisting of WM-62, WM-415, WM-152, WM-385, WM-347, WM-134, WM-36, WM-108, WM-99, WM-151, WM-289, WM-363, WM-61, WM-117, and WM-211.
- 62. The method according to claim 60, wherein the protein is selected from the group consisting of WM-62, WM-415, WM-152, WM-385, and WM-347.
- 63. A kit for distinguishing lung adenocarcinoma from squamous lung carcinoma, comprising
- (A) an adsorbent attached to a substrate that retains one or more of the biomarkers WM-16, WM-26, WM-499, WM-134, WM-647, WM-277, WM-310, WM-363, WM-446, WM-221, WM-648, WM-657, WM-290, WM-328, WM-447, WM-684, WM-183, WM-190, WM-686, WM-397, WM-466, WM-20, WM-17, WM-545, WM-47, WM-191, WM-147, WM-480, WM-590, WM-218, WM-285, WM-652, WM-651, WM-366, WM-403, WM-418, WM-430, WM-456, WM-714, WM-646, WM-109, WM-302, WM-587, WM-375, WM-131, WM-706, WM-398, WM-309, WM-55, and WM-488, and
- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- 64. A kit according to claim 63, further comprising a washing solution or instructions for making a washing solution.
- 65. A kit according to claim 63, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.
- 66. A method for distinguishing lung adenocarcinoma from small cell lung carcinoma in a subject, comprised of analyzing a biological sample from said subject

for a level of a protein selected from the group consisting of WM-457, WM-72, WM-369, WM-78, WM-79, WM-73, WM-64, WM-320, WM-419, WM-85, WM-82, WM-53, WM-412, WM-440, WM-455, WM-313, WM-456, WM-86, WM-70, WM-246, WM-360, WM-190, WM-418, WM-83, WM-257, WM-138, WM-47, WM-252, WM-282, WM-60, WM-68, WM-325, WM-402, WM-411, WM-405, WM-75, WM-417, WM-387, WM-26, WM-410, WM-420, WM-164, WM-67, WM-66, WM-391, WM-340, WM-428, WM-198, WM-312, and WM-152.

- 67. The method according to claim 66, wherein the protein is selected from the group consisting of WM-457, WM-72, WM-369, WM-78, WM-79, WM-73, WM-64, WM-320, WM-419, WM-85, WM-82, WM-53, WM-412, WM-440, and WM-455.
- 68. The method according to claim 66, wherein the protein is selected from the group consisting of WM-457, WM-72, WM-369, WM-78, and WM-79.
- 69. A method for distinguishing lung adenocarcinoma from small cell lung carcinoma in a subject, comprising
- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- (B) extracting data from the spectrum and subjecting the data to pattern-recognition analysis that is keyed to at least one peak selected from either a first group consisting of WM-457, WM-72, WM-369, WM-78, WM-79, WM-73, WM-64, WM-320, WM-419, WM-85, WM-82, WM-53, WM-412, WM-440, WM-455, WM-313, WM-456, WM-86, WM-70, WM-246, WM-360, WM-190, WM-418, WM-83, WM-257, WM-138, WM-47, WM-252, WM-282, WM-60, WM-68, WM-325, WM-402, WM-411, WM-405, WM-75, WM-417, WM-387, WM-26, WM-410, WM-420, WM-164, WM-67, WM-66, WM-391, WM-340, WM-428, WM-198, WM-312, and WM-152.
- 70. The method according to claim 69, wherein the protein is selected from the group consisting of WM-457, WM-72, WM-369, WM-78, WM-79, WM-73, WM-64, WM-320, WM-419, WM-85, WM-82, WM-53, WM-412, WM-440, and WM-455.

- 71. The method according to claim 69, wherein the protein is selected from the group consisting of WM-457, WM-72, WM-369, WM-78, WM-79.
- 72. A kit for distinguishing lung adenocarcinoma from small cell lung carcinoma, comprising
- (A) an adsorbent attached to a substrate that retains one or more of the biomarkers WM-276, WM-277, WM-362, WM-257, WM-363, WM-347, WM-53, WM-254, WM-17, WM-252, WM-431, WM-513, WM-446, WM-355, WM-447, WM-133, WM-245, WM-52, WM-96, WM-238, WM-243, WM-138, WM-62, WM-580, WM-134, WM-240, WM-256, WM-203, WM-111, WM-95, WM-247, WM-157, WM-242, WM-556, WM-63, WM-239, WM-234, WM-274, WM-370, WM-301, WM-449, WM-74, WM-261, WM-467, WM-237, WM-262, WM-295, WM-288, WM-384, and WM-37, and
- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- 73. A kit according to claim 72, further comprising a washing solution or instructions for making a washing solution.
- 74. A kit according to claim 72, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.
- 75. A method for distinguishing squamous cell lung carcinoma from small cell lung carcinoma in a subject, comprised of analyzing a biological sample from said subject for a level of a protein selected from the group consisting of WM-276, WM-277, WM-362, WM-257, WM-363, WM-347, WM-53, WM-254, WM-17, WM-252, WM-431, WM-513, WM-446, WM-355, WM-447, WM-133, WM-245, WM-52, WM-96, WM-238, WM-243, WM-138, WM-62, WM-580, WM-134, WM-240, WM-256, WM-203, WM-111, WM-95, WM-247, WM-157, WM-242, WM-556, WM-63, WM-239, WM-234, WM-274, WM-370, WM-301, WM-449, WM-74, WM-261, WM-467, WM-237, WM-262, WM-295, WM-288, WM-384, and WM-37.
- 76. The method according to claim 75, wherein the protein is selected from the group consisting of WM-276, WM-277, WM-362, WM-257, WM-363, WM-347, WM-53, WM-254, WM-17, WM-252, WM-431, WM-513, WM-446, WM-355, and WM-447.

- 77. The method according to claim 75, wherein the protein is selected from the group consisting of WM-276, WM-277, WM-362, WM-257, and WM-363.
- 78. A method for distinguishing squamous cell lung carcinoma from small cell lung carcinoma in a subject, comprising
- (A) providing a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, and
- (B) extracting data from the spectrum and subjecting the data to pattern-recognition analysis that is keyed to at least one peak selected from either a first group consisting of WM-276, WM-277, WM-362, WM-257, WM-363, WM-347, WM-53, WM-254, WM-17, WM-252, WM-431, WM-513, WM-446, WM-355, WM-447, WM-133, WM-245, WM-52, WM-96, WM-238, WM-243, WM-138, WM-62, WM-580, WM-134, WM-240, WM-256, WM-203, WM-111, WM-95, WM-247, WM-157, WM-242, WM-556, WM-63, WM-239, WM-234, WM-274, WM-370, WM-301, WM-449, WM-74, WM-261, WM-467, WM-237, WM-262, WM-295, WM-288, WM-384, and WM-37.
- 79. The method according to claim 78, wherein the protein is selected from the group consisting of WM-276, WM-277, WM-362, WM-257, WM-363, WM-347, WM-53, WM-254, WM-17, WM-252, WM-431, WM-513, WM-446, WM-355, and WM-447.
- 80. The method according to claim 78, wherein the protein is selected from the group consisting of WM-276, WM-277, WM-362, WM-257, and WM-363.
- 81. A kit for distinguishing squamous cell lung carcinoma from small cell lung carcinoma, comprising
- (A) an adsorbent attached to a substrate that retains one or more of the biomarkers WM-276, WM-277, WM-362, WM-257, WM-363, WM-347, WM-53, WM-254, WM-17, WM-252, WM-431, WM-513, WM-446, WM-355, WM-447, WM-133, WM-245, WM-52, WM-96, WM-238, WM-243, WM-138, WM-62, WM-580, WM-134, WM-240, WM-256, WM-203, WM-111, WM-95, WM-247, WM-157, WM-242, WM-556, WM-63, WM-239, WM-234, WM-274, WM-370, WM-301, WM-449, WM-74, WM-261, WM-467, WM-237, WM-262, WM-295, WM-288, WM-384, and WM-37, and

- (B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.
- 82. A kit according to claim 81, further comprising a washing solution or instructions for making a washing solution.
- 83. A kit according to claim 81, wherein the substrate is a SELDI probe that comprises functionalities that allow for cation exchange.
- 84. Software for qualifying lung carcinoma status in a subject, comprising an algorithm for analyzing data extracted from a spectrum generated by mass spectroscopic analysis of a biological sample taken from the subject, wherein said data relates to one or more biomarkers selected from either a first group consisting of
- (i) IM-522, IM-273, IM-520, IM-519, IM-454, IM-507, IM-521, IM-148, IM-266, IM-537, IM-471, IM-510, IM-544, IM-474, IM-155, IM-157, IM-176, IM-445, IM-177, IM-440, IM-468, IM-438, IM-547, IM-359, IM-436, IM-106, IM-455, IM-444, IM-158, IM-265, IM-50, IM-159, IM-156, IM-439, IM-157, IM-508, IM-514, IM-478, IM-473, IM-360, IM-435, IM-150, IM-151, IM-110, IM-51, IM-163, IM-437, IM-546, IM-153, and IM-268,

or from a second group consisting of

- (ii) WM-61, WM-447, WM-446, WM-133, WM-119, WM-278, WM-134, WM-363, WM-282, WM-362, WM-120, WM-290, WM-65, WM-277, WM-70, WM-369, WM-17, WM-473, WM-47, WM-203, WM-276, WM-279, WM-62, WM-366, WM-456, WM-428, WM-384, WM-287, WM-420, WM-292, WM-431, WM-455, WM-20, WM-340, WM-105, WM-389, WM-63, WM-354, WM-450, WM-466, WM-296, WM-343, WM-341, WM-339, WM-55, WM-66, WM-48, WM-38, WM-138, and WM-310.
- 85. Software according to claim 84, wherein said algorithm carries out a pattern-recognition analysis that is keyed to data relating to at least one of the biomarkers.
- 86. Software according to claim 85, wherein said algorithm comprises classification tree analysis that is keyed to data relating to at least one of the biomarkers.

- 87. Software according to claim 85, wherein said algorithm comprises artificial neural network analysis that is keyed to data relating to at least one of the biomarkers.
- 88. A method for qualifying lung carcinoma status in a subject, comprised of analyzing a biological sample from said subject for a diagnostic level of a biomarker that is serum amyloid A protein or a fragment thereof.
- 89. A method according to claim 88, wherein said serum biomarker has an apparent molecular weight of about 2803, 3168, 3277, 3552, 3897, 4300, 4490, 4655, 5927, 6874, 7776, 7941, 8152, 8952, 9233, 10300, 10866, or 10851 Daltons.
- 90. A method according to claim 89, wherein said serum biomarker has an apparent molecular weight of about 3168, 3277, 3552, 3897, 4300, 4490, 4655, 7776, 7941, 8152, 8952, or 10851 Daltons:
- 91. A method according to claim 88, wherein said serum biomarker has an apparent molecular weight of about 11.5 to 11.7 kD.
- 92. A method according to claim 88, for qualifying risk of lung adenocarcinoma.
- 93. A method according to claim 88, for qualifying risk of squamous cell lung carcinoma.
- 94. A method according to claim 88, for qualifying risk of small cell lung carcinoma.
- 95. A method according to claim 88, for qualifying risk of non-small cell lung carcinoma.
- 96. A method according to claim 88, for qualifying risk of large cell lung carcinoma.
 - 97. A kit for detecting and diagnosing lung carcinoma, comprising
- (A) an adsorbent attached to a substrate that retains one or more of the biomarkers that are serum amyloid A protein or a fragment thereof.

and

(B) instructions to detect the biomarker(s) by contacting a sample with the adsorbent and detecting the biomarker(s) retained by the adsorbent.

- 98. A kit according to claim 97, wherein said serum biomarker has an apparent molecular weight of about 2803, 3168, 3277, 3552, 3897, 4300, 4490, 4655, 5927, 6874, 7776, 7941, 8152, 8952, 9233, 10300, 10866, or 10851 Daltons.
- 99. A kit according to claim 98, wherein said serum biomarker has an apparent molecular weight of about 3168, 3277, 3552, 3897, 4300, 4490, 4655, 7776, 7941, 8152, 8952, or 10851 Daltons.
- 100. A kit according to claim 97, wherein said serum biomarker has an apparent molecular weight of about 11.5 to 11.7 kD.
- 101. A kit according to claim 97, further comprising a washing solution or instructions for making a washing solution.
 - 102. A kit according to claim 97, wherein the substrate is a SELDI probe.

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IM-309	2144	۵ ۵	IM-345	3725	۵	IM-381	80844	۵	IM-417	2612	ш
IM-310	2154	۵ ۵	IM-346	3833	۵	IM-382	88962	۵	IM-418	2662	ш
IM-311	2166	Ω	IM-347	3899	Δ	IM-383	94399	۵	IM-419	2723	w
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IM-314	2231	۵ ۵	IM-350	4297	۵	IM-386	116433	۵	IM-422	2849	ш
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IM-319	2412	۵	IM-355	7977	۵	IM-391	159524	۵	IM-427	3319	ш
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IM-321	2466	۵	IM-357	8139	۵	IM-393	2010	ш	IM-429	3693	ш
IM-322	2480	۵	IM-358	9292	۵	IM-394	2029	ш	IM-430	3731	Ш
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מו משאמאאו	1 A 460	804-MI	IM-470	1.74-MI	IM-472	IM-473	IM-474	IM-475	IM-476	IM-477	IM-478	IM-479	IM-480	IM-481	IM-482	IM-483	IM-484	IM-485	IM-486	IM-487	IM-488	IM-489	IM-490	IM-491	IM-492	IM-493	IM-494	IM-495	IM-496	IM-497	IM-498	IM-499	IM-500	IM-501	IM-502	IM-503	IM-504
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9	4473	IM-507	4	2967	IM-110
7	13887	IM-521	45	6122	IM-51
ထ	5272	IM-148	46	6958	IM-163
Ō	5365	IM-266	47	4355	IM-437
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7	132843	IM-474			
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23	100310	IM-542			
24	11671	IM-359			
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27	13910	IM-455			
58	2985	IM-444			
53	5988	IM-158			
30	5347	IM-265			
31	5918	IM-50			
32	6137	IM-159			
33	5916	IM-156			
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Figure 38

igure 3C

78803	99969	24583	100082	10/05	110601	117940	132612	145083	158971	175363	197052	2010	2032	8/87	34.65	200	2,50		262	Š	2430	2474	883	2562	2837	1512	2856	2835	3083	- :	358	3282		900F		2637		4130	4211	4207	4410	4801	6832	3777	8152	9195	9288	3
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78804	89215	94578	99666	107086	110309	117925	132591	144894	158780	174503	197425	2011	2032	2077	2166	2183	2212	8222	2276	2302	2355	2431	7842	2505	2849	2757	2884	2833	3060	3144	3168	3280	3460	3565	3686	3813	7 2 3	\$C#0	7007				6616	7751	8174	, LZZ8		11697
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igure 3D

14069	15139	15888	9000	00777	82102	orone orone	3/2/0	96010	67475	21288	98338	B 15	24607	1907	0000	90400	09089	94738	89786	110815	118344	132435	145594	155075	165437	176871	197015	2012	2033	2054	2070	2167	2783	2238	2255	2278	2288	2354	2428	2481	2486		2637	2750	2884	500
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14086	15139	15887	17337	22248	28110	33314	37236	44542	47384	51237	96299	59758	66463	74850	76808	90557	93209	96814	80700	410826	118217	132417	145477	155075	165431	177058	106011	2010	2032	2053	2078	2169	š	127	2755	2278	6822	2352	2427	2480	5500	2542	2637	27.48	7 000	7804
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14078	15138	15882	17376	22250	28129	33326	37215	44515	47399	51284 ::	26280	59738	. 66443	74702	78738	80375	83617	2/890	2400	110705	11837	132417	145642	154931	165399	177208	107005	2010	2032	2063	2080	2167	2184	2272	2756	722	2300	2364	2428	2483	2500	2531	2837	2764	1000	/WW/
14080	15148	15668	17367	22258	28123	2222	37276	44513	47424	51290	66240	69764	68443	74685	78889	80450	83698	18889	20143	410884	118298	132440	145781	154787	165442	177380	197088	2011	2032	2002	2078	2167	2185	12 K	355	22	2298	2363	2428	2480	2780	2543	2637	2749		2257
14088	15141	15870	17337	22250	28117	32316	37214	44528	47378	61236	26280	59763	68445	74914	78819	80408	83637	88828	01/4	440758	118183	132397	145087	154930	166378	177184	10888	2010	2032	2054	0702	2167		2122	25.5	LIZZ	8672	2354	2428	2481	2490	2538	2837	2751	2006	0097
14083 東西西	15148 (25/27)	16882	17305 (2)	22228 (2005)	28110	33310 Marie	37250	44511	47380旅船	51Z10	56.20 to	50781	86438 FE	74749 24	78018	80232	83685	20017	200	2000		132423 125	145134 (20)	154912、公司	186497	17308 23	101213131313131	2011	2032	202 E02	2078	2168日次至日	2188			2778	2302 FF 65	2367	2427 (2022)	2483 氏公司	2500	25	2578 2578		10000	27500 F. TOWNS
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WM-204 C	WALZOS C	WM-206 C	WM-207 C		WA-209 C	WAR-ZIO C		WW-212 C		WM-214 C	WM-215 C	_	WW-217 C	WW-218 C			WM-221 C	WW-222		WIL225 C		WM-227 C		WM-229 C	WM-230 C	WM-231 C	_	WM-234 D	WM-235 D				WM-239 D	_								WW-249 D	WM-251 D			

Figure 3E

3083	0000	2826	130F	4	3557	3888	3814	1 88	3950		4130	4208	0144	47785	6437	6630	6948	7673	7384	7847	11497	11679	13773	13882	U4161	15888	1/340	28135	33387	37232	40280	41190	44588	61262	. 58887	2000	08001	78103	80423	81850	88035	94543	99733	107159	110405	117271	132469	145819
3083	4010	3284	3370	3448	3559	3688	3816	3842	3951	4051	4123	4208		4796	6437	9639	1509	7572	7768	7948	11500	11693	13774	13869	15137	15885	1131	28148	34555	37278	40320	41162	44558	51238	59655	9440	13/12	7,804.3	1004 1004 1004 1004 1004 1004 1004 1004	3	88840	94514	99820	107188	110341	117416	132451	145763
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Figure 3F

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		160431	175807	182180	. 2011	2028	2062	2067	2001		2168	2166	242		8/22	2		2481	2489	2587	2581		52000	3158	25.5	2447	388	4055		4211	4259	4358	9 4 ;	2	629	1901	5070			6643	9259	9886		787 787	200	1028
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Figure 36

	8830	8968	9494	8808	7.78	11527	11718	12459	8,00		1308/	15154	15896	17385	22332	28172	33428	38238	44675	51409	59799	66604	75413	78327	88361	100001	109921	117465	132842	146853	152534	165575	183356	100	2 2	8707	2087	2080	2128	2166	2213	2334	6,22	8827		2412	2482	2200	900	7907	
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2722 2760 2866 2878 3162 3458 3458 3458 3558 3717	4054 4155 4212	4376 4473 4828 4831 5883 6449	6488 6848 6847 7182 7771 7771 8231 6701	8831 8855 8855 8855 8171 8467 11736 11736 11506 117350 17350	28194
2772 2752 2868 2970 2970 2971 3489 3489 3117	4055 4155 4215 4215	4261 4216 4419 4471 4630 4638 6683 6451	0483 0659 0649 7183 7777 7951 8786	8870 8870 8871 8477 1158 11728 12822 13808 14038 15158 15158 15158 15240 15289 17288	28190
2772 2751 2865 2865 2876 3971 3439 3439 3468 3578	4054 4154 4204 4216	4420 4473 4830 4837 6848 6448	6494 6650 6650 6650 6968 7777 7772 8761 8761	9570 9678 9771 9776 11565 11739 12461 14101 15101 1534 17286 17391 23350	28195
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2722 2751 2667 2667 2667 2667 2758 3472 8441 8441	4054 4156 4203	4574 4474 4478 4630 4831 5863	0465 6845 6847 7161 7777 7849 8239	68708 6851 6851 11737 11737 11737 11508 12503 12503 1251 1251 1251 12509 12509 12509	28180
2772 2751 2761 2865 2870 2871 3871 3876 3876 3876 3876 3876	4057 4154 4179 4189 4218	638 4421 4421 4631 848 848	9446 9650 9654 7202 7600 7774 8244	8878 8884 8174 9175 11653 1172 12828 12828 15938 1683 17313 17313 17313	20215
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33468	43393	44688	51189	56517	59495	68570	76313	79194		89568	94765	100355	116983	132756	148862	160793	2131							2992					2120	3		2982			308							4214	*17 .	4529	
33504	25.5	44758		56410	58644	80990	76561	78348	88331	89751	84626	100614	117130	132640	148960			2184	. 2414				. 2568								2978			3033				-				4414	2		
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Figure 3 M

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Rank	Normal vs Cancer	Adeno vs Normal	Squamous vs Normal Smail Cell vs Normal	Small Cell vs Normal	Non-small Cell vs Normal	Large Cell vs Normal	Adeno vs Squamous Adeno vs Small Gell	Adeno vs Small Cell	Squamous vs Small Celi
-	WM-61	WM-447	WM-447	WM-70	WM-341 .	WM-16	WM-62	WM-457	WM-276
~	WW-447	WM-652	WM-61	WM-706	WM-342	WM-26	WM-415	WM-72	WM-277
6	WM-446	WM-61	WM-277	WM-359	WM-343	WM-489	WM-152	WM-369	WM-362
4	WN4-133	WM-446	WM-446	WM-447	WM-48	WM-134	WM-385	WM-78	WM-257
S	WM-119	WM-290	WM-133	WM-61	WM-340	WM-647	WM-347	WM-79	WM-363 .
9	WM-278	WM-363	WM-134	WM-652	WM-346	WM-277	WM-134	WM-73	WM-347
7	WM-134	WM-133	WM-363	WM-282	WM-47	WM-310	WM-36	WM-64	WM-53
89	WM-383	WM-341	WM-362	WM-446	WM-339	WM-363	WM-108	WM-320	WM-254
01	WM-282	WM-285	WN-276	WM-456	WW-389	WM-446	WM-99	WM-419	WM-17
9	WM-362	WM-366	WM-706	WM-134	WM-669	WM-221	WM-151	WM-85	WM-252
F	WM-120	WM-282	WM-203	WM-203	WM-447	WM-648	WM-289	WM-82	WM-431
12	WM-290	WM-362	WW-468	WM-646	WM-652	WM-657	WM-363	WM-53	WM-513
13	WM-65	WM-310	WW-366	WM-455	WM-154	WM-290	WM-61	WW-412	WM-446
7	WM-277	WM-292	WN-65	WM-65	WM-587	WM-328	WM-117	WM-440	WM-355
15	WM-70	WM-120	WM-70	WM-685	WW-456	WM-447	WM-211	WW-455	WM-447
16	WM-369	WM-134	WAF-341	WM-473	WM-450	WM-684	WM-362	WM-313	WM-133
1	WM-17	WM-276	WN-429	WM-343	WM-283	WM-183	WM-133	WM-458	WM-245
18	WM-473	WM-428	WM-347	WM-456	WW-207	WM-190	WM-414	WW-86	WM-52
19	WM-47	WM-277	WA-17	WM-341	WM-436	WM-686	WM-277	WM-70	WM-86
æ	WM-203	WM-20	WW-47	WM-340	WM-384	WM-397	WM-141	WM-246	WM-238
71	WM-276	WM-119	WM-431	WM-363	WM-61	WM-466	WM-64	WM-360	WM-243
a	WM-279	WM-340	WM-62	WM-339	WM-167	WM-20	WM-135	WM-180	WM-138
Ø	WM-62	WM-48	WM-473	WM-457	WM-382	WM-17	WM-447	WM-418	WM-62
2	WM-366	WM-389	WM-384	WM-86	WM-285	WM-545	WM-383	WM-83	WM-580
z	WM-456	WM-450	WM-438	WM-506	WM-650	WM-47	WM-338	WM-257	WM-134
8	WM-428	WM-47	WM-652	WIM-72	WM-203	WM-191	WM-63	WM-138	WM-240
22	WM-384	WM-343	WM-282	WM-287	WJ-119.	WM-147	WM-142	WW-47	WM-258
82	WM-287	WM-17	WM-389	WM-82	WM-282	WM-480	WM-446	WM-252	WM-203
29	WM-420	WM-583	WM-290	WM-528	WM-686	WM-590	WM-186	WM-282	WM-111
8	WM-292	WM-70	WM-278	WM-85	WM-383	WM-218	WM-111	WM-50	WM-95
F	WM-431	WM-706	WM-456	WM-73	WM-429	WM-285	WM-445	WM-68	WM-247
R	WM-455	WM-346	WM-673	WM-138	WM-11	WM-652	WM-455	WM-325	WM-157
33	WM-20	WM-466	WM-340	WM-384	WM-208	WM-651	WM-276	WM-402	WM-242
34	WM-340	WM-646	WM-55	WM-83	WM-451	WM-368	WM-444	WM-411	WM-556
35	WM-19	WM-384	WM-455	WM-450	WM-473	WM-403	WM-181	WM-405	WM-63
36	WM-389	WM-338	WM-645	WM-310	WM-220	WM-418	WM-35	WM-75	WM-239
37	WM-63	WM-294	WM-138	WM-277	WM-685	WM-430	WM-285	WM-417	WM-234
38	WM-438	WM-339	WM-420	WM-79	WM-338	WM-456	WM-456	WM-387	WM-274

						5				
9	WM-450	WM-473	WM-450	WM-207	WM-71	WM-714	DE-MAN	WAA.28	WW.370	
9	WM-468	WM-369	WM-369	WM-278	WM-268	WW-545	WW.R2	WW. 440	WAR 304	
<u>.</u>	WM-296	WM-38	WM-279	WW-290	WW-70	WW-109	VAR-17	WAY AD	WALAAO	
23	WM-343	WM-283	WM-342	WM-366	WM-545	WW-302	VAINT-203	140 1EA	WIN-440	
9	WM-341	WM-685	WM-471	WM-472	WM-675	WM-587	WW-EG	MAN 97	+3C 1001	
3	WM-339	WM-65	WM-674	WW-420	WM-448	WAA-375	WAL 412	WINECO	107-JANA	
Į.	WM-55	WM-65	WM-120	WW4-147	WW.120	WW.181	WIN OF	WINFOU.	104-101	
9	WM-66	WM-650	WW-20	WM-55	WW.267	WAY TOB	WAY 74	WWF331	140.4 DES	
2	WM-48	WM-307	WM-287	WW-669	WM-468	WW.308	VAN 487	WWF34U	WW-202	
80	WM-38	WM-278	WM-83	WM-357	WM-347	WW.369	WW.431	WMA	CEZ-MAA	
6	WM-138	WM-342	WM-154	WM-429	WM-153	WM-55	WW-340	WALSTS	WW-200	
0	WM-310	WM-429	WM-128	WM-279	WM-38	WW.48R	WW-49	WWF312	WWC0+	

gure 4B

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SAA 42-67 (2802.1) 3168 SAA 69-97 (3167.3)	5927 SAA 32- <u>85</u> (5925.3)	10300 SAA 6-97 (10299 1)
3277 SAA 39-68 (3276.6)	6874 SAA 26-88 (6873.3)	10866
3552 SAA 38-70 (3552)	7776 SAA 1-68 (7774.6)	SAA 4-101 (10871.8)
3897 SAA 64-98 (3897.2)	7941 SAA 18-88 (7939.5)	SAA 5-102 (10853.7)
4300 SAA 54-93 (4302.5)	8152 SAA 25-98 (8150)	
4490 SAA 53-93 (4489)	8952 SAA 6- <u>85</u> (8950)	
4655 SAA 5-44 (4655.0)	9233 SAA 16- <i>97</i> (9235)	Figure 5

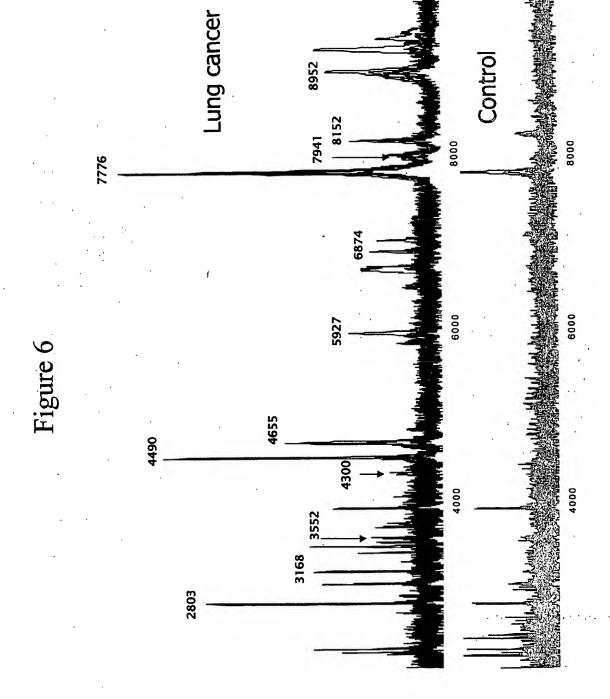
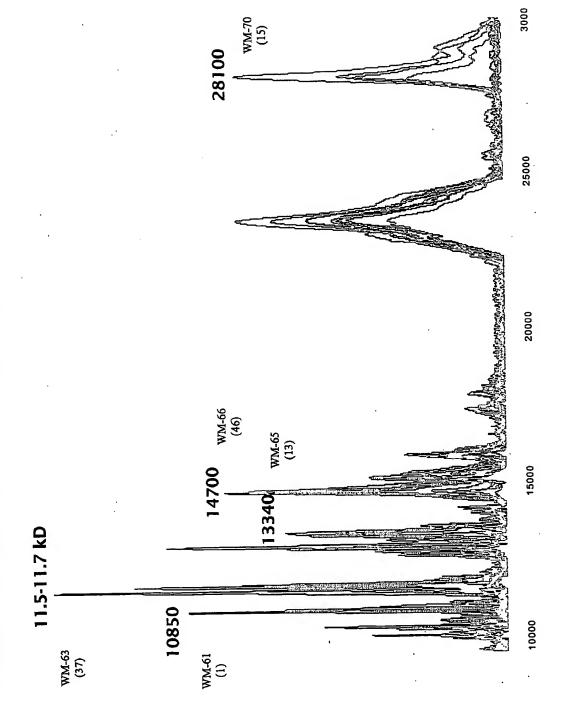
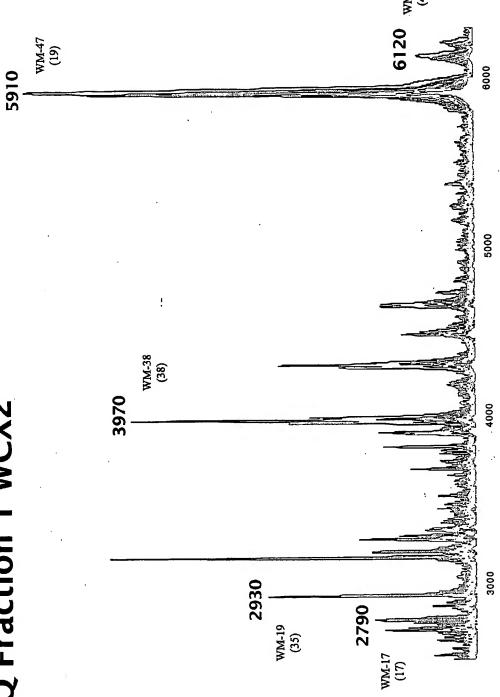


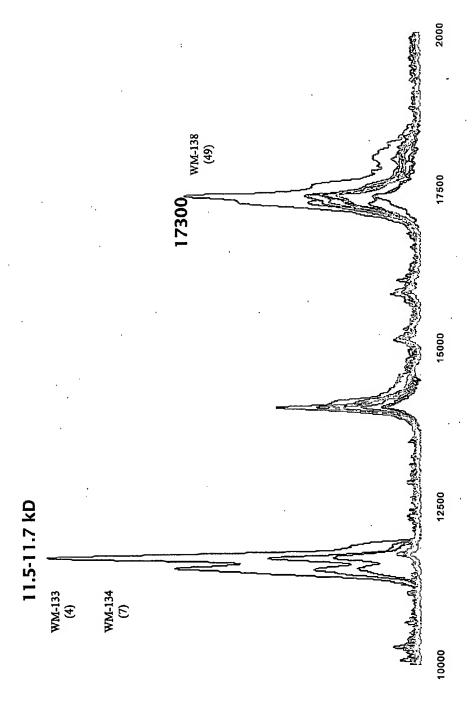
FIGURE 7 Protein Profile of Selected Samples Q Fraction 1 WCX2



Protein Profile of Selected Samples Q Fraction 1 WCX2 Figure 8



Protein Profile of Selected Samples Q Fraction 2 WCX2 Figure 9



Protein Profile of Selected Samples Q Fraction 2 WCX2 Figure 10

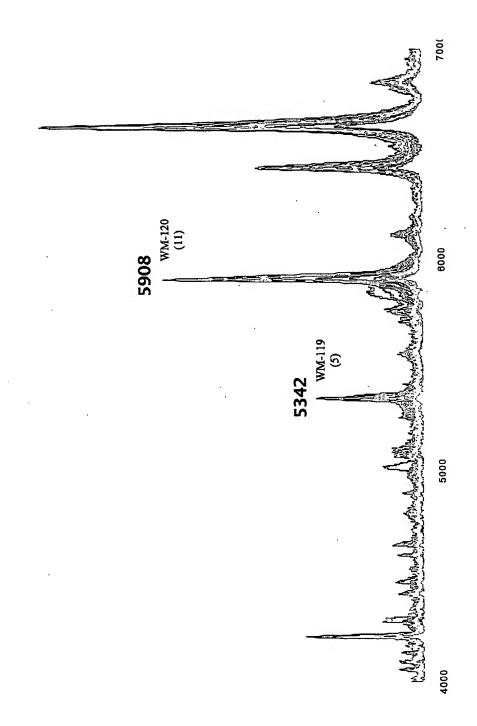


Figure 11 Protein Profile of Selected Samples Q Fraction 4 WCX2 13.8-13.9 kD

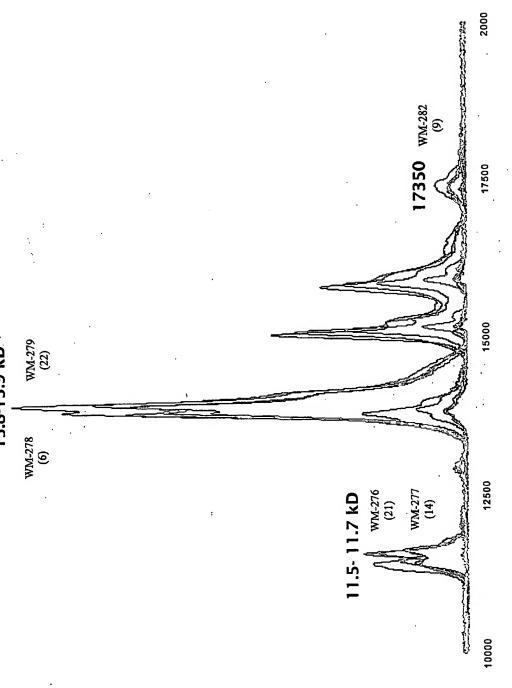


Figure 12
Protein Profile of Selected Samples
Q Fraction 4 WCX2
66.5 kD

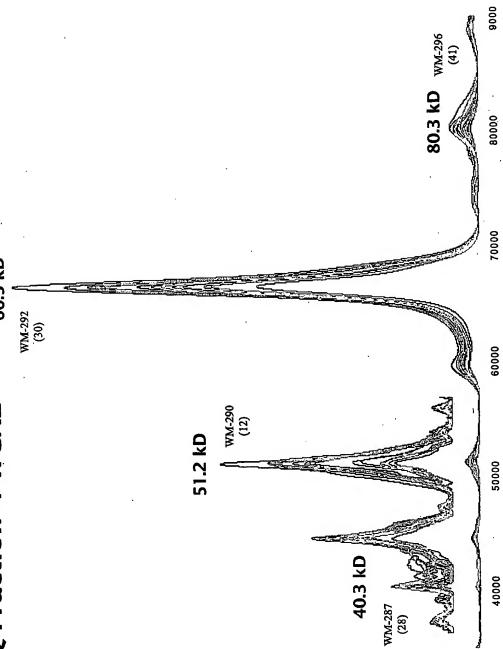


Figure 13 Protein Profile of Selected Samples Q Fraction 5 WCX2

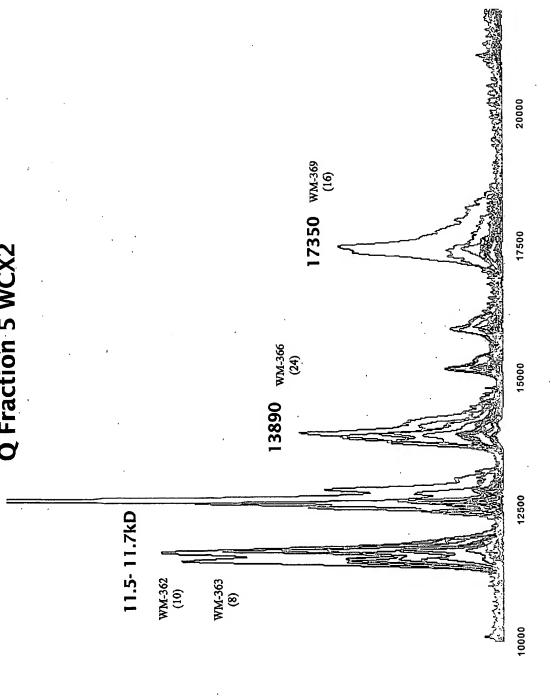
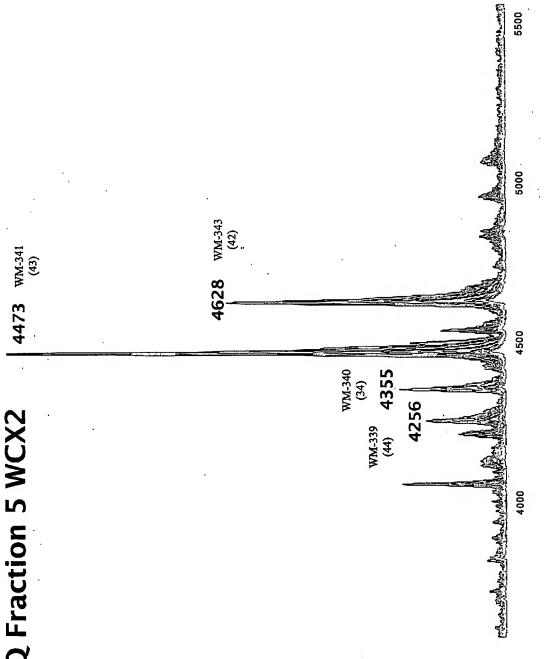
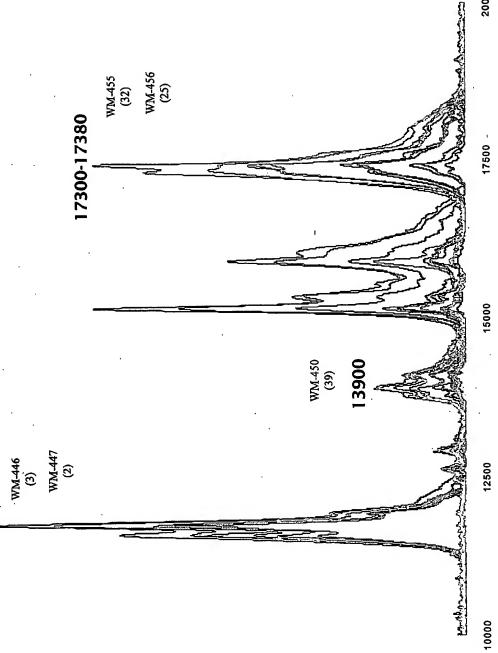


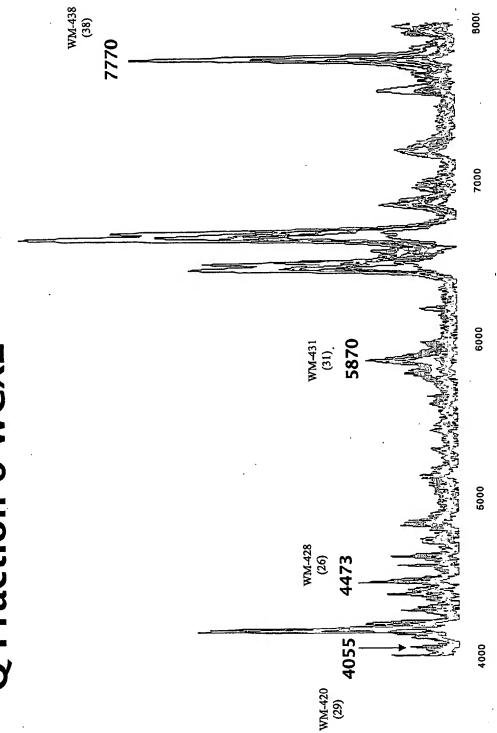
Figure 14
Protein Profile of Selected Samples
Q Fraction 5 WCX2 | 4473 WM.341



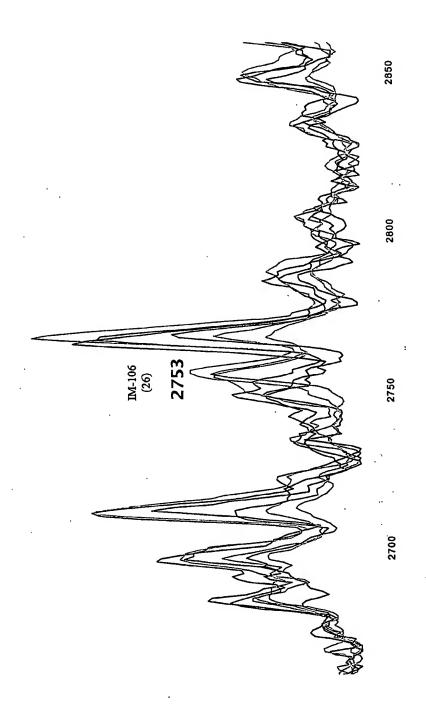
Q Fraction 6 WCX2 Figure 15 Protein Profile of Selected Samples



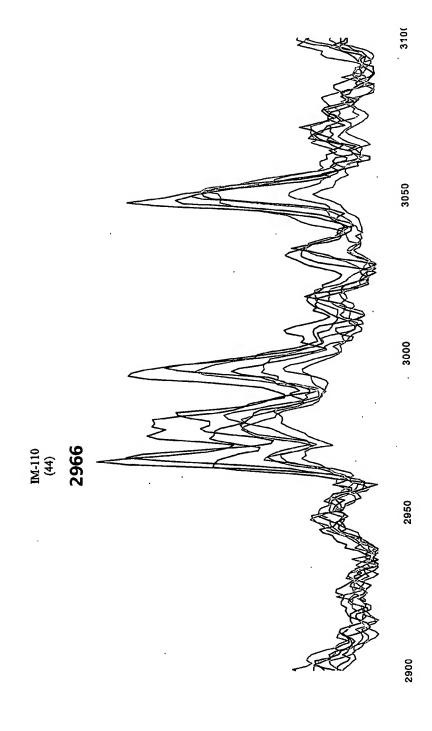
Protein Profile of Selected Samples Q Fraction 6 WCX2 Figure 16



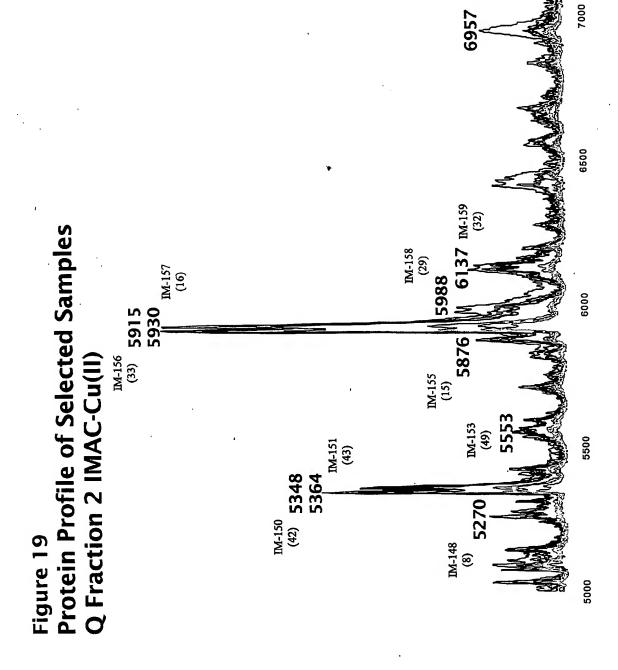
Protein Profile of Selected Samples Q Fraction 2 IMAC-Cu(II) Figure 17

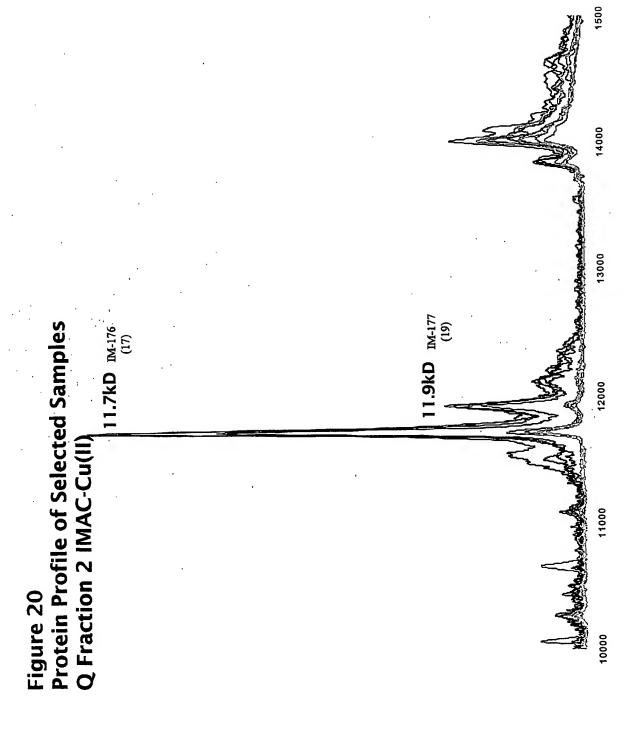


Protein Profile of Selected Samples Q Fraction 2 IMAC-Cu(II) Figure 18

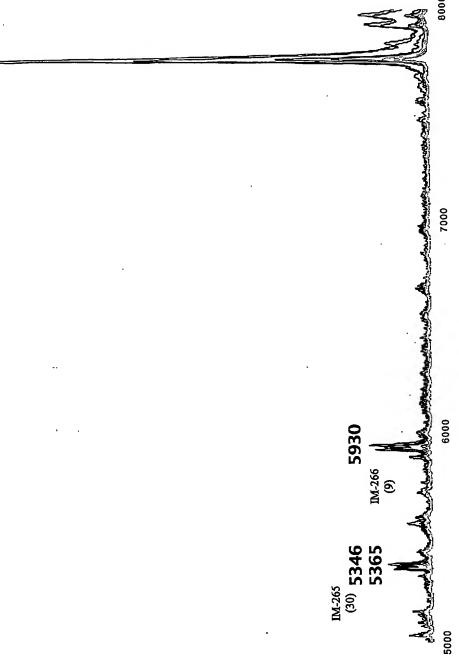


IM-163 (46)

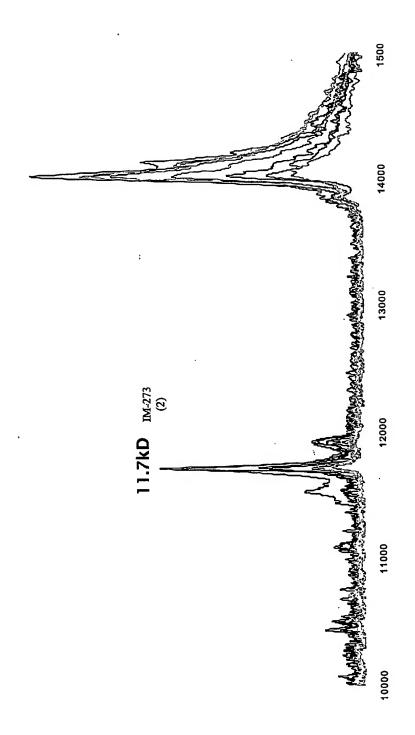


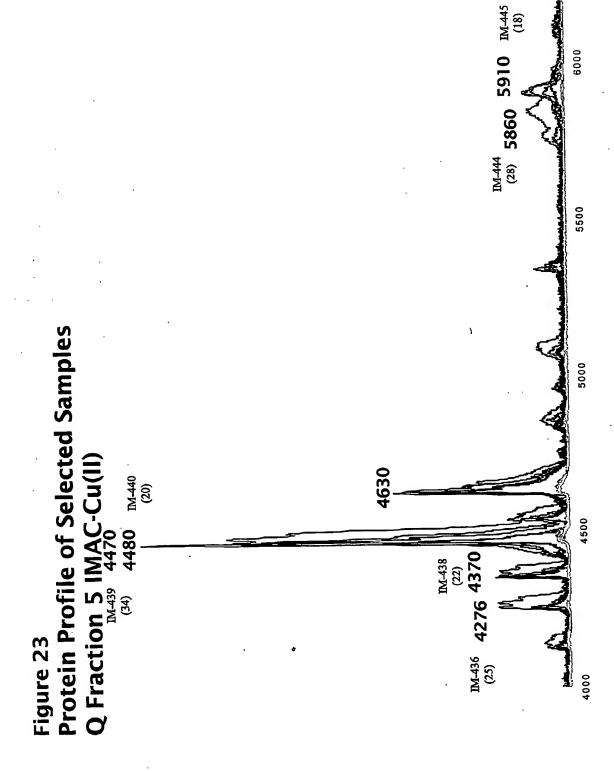




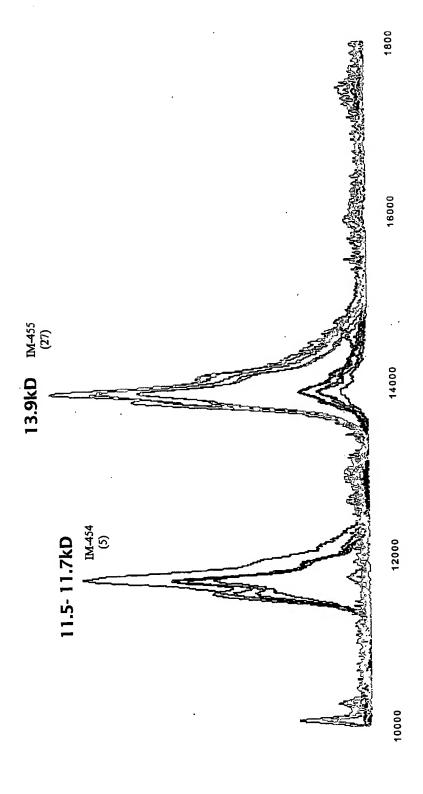


Protein Profile of Selected Samples Q Fraction 3 IMAC-Cu(II) Figure 22





Protein Profile of Selected Samples Q Fraction 5 IMAC-Cu(II) Figure 24



IM-478 (38) 176600 175000 150000 Figure 25
Protein Profile of Selected Samples
Q Fraction 5 IMAC-Cu(II) IM-474 (14) 125000 IM-473 (39) 117100 100300 100000 IM-471 (11) 79450 IM-468 (21) 75000

Protein Profile of Selected Samples Q Fraction 6 IMAC-Cu(II) Figure 26

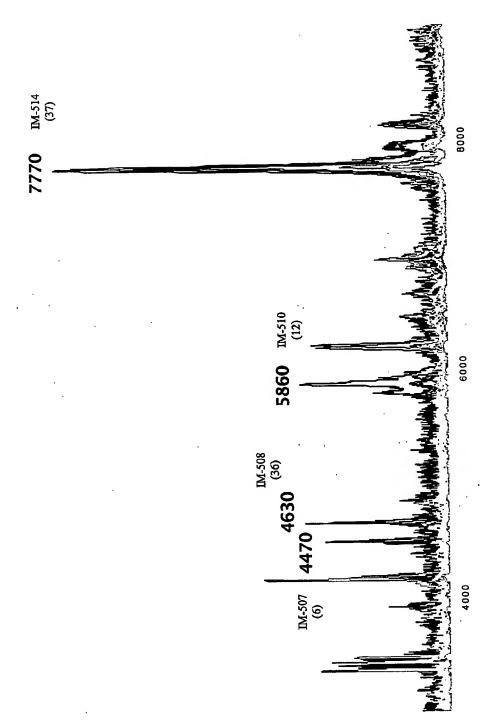


Figure 27 Protein Profile of Selected Samples Q Fraction 6 IMAC-Cu(II)

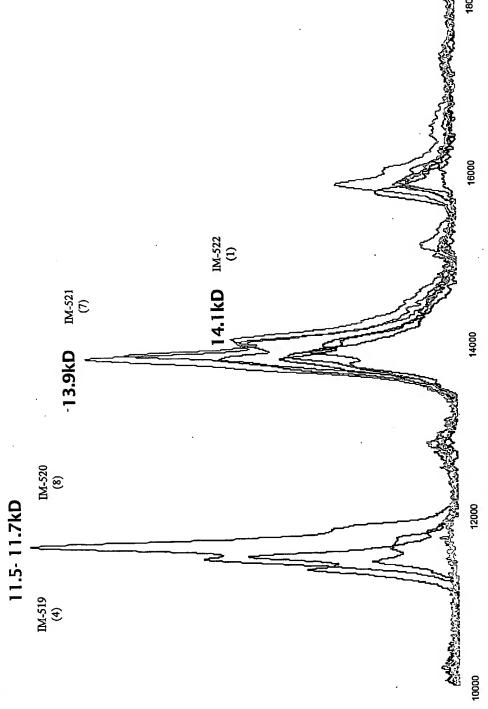
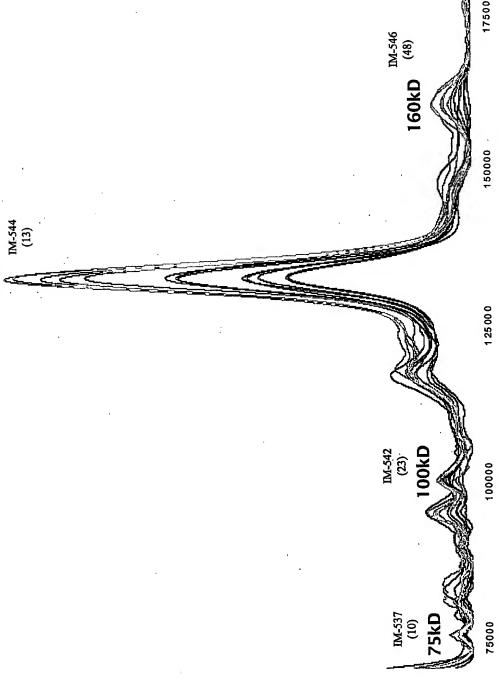


Figure 28
Protein Profile of Selected Samples
Q Fraction 6 IMAC-Cu(II)



(19) World Intellectual Property Organization

International Bureau



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(71) Applicants (for all designated States except US): CI-PHERGEN BIOSYSTEMS, INC. [US/US]; 6611 Dumbarton Circle, Freemont, CA 94555 (US). QUEEN ELIZABETH HOSPITAL [CN/CN]; 30 Gascoigne Road, Kowloon, Hong Kong SAR (CN).

(72) Inventors; and

(75) Inventors/Applicants (for US only): YIP, Timothy, Tak, Chun [CN/CN]; 1, Kapok Path, Westwood, Palm Springs, Yuen Long N.T., Hong Kong SAR (CN). CHO, Chi, Shing [-/CN]; Flat 9E, Block 4, The Tolo Place, Sunshine City, Ma On Shan, N.T., Hong Kong SAR (CN). AU, Siu, Kie [--/CN]; c/o Department of Clinical Oncology, Queen Elizabeth Hospital, 30 Gascoigne Road, Kowloon, Hong Kong SAR (CN). YIP, Tai-Tung [US/US]; 1532 Aster Court, Cupertino, CA 95014 (US). YIP, Christine, L. [US/US]; 1532 Aster Court, Cupertino, CA 95014 (US). YIP, Victor, F. [US/US]; 33008 Compton CT, Union City, CA 94587 (US).

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International application No.

PCT/US03/37090

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B. FIELDS SEARCHED							
Minimum documentation searched (classification system followed by classification symbols) U.S.: 435/4; 435/7.1; 424/9.1							
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C. DOCUMENTS CONSIDERED TO BE RELEVANT							
Category *	Citation of document, with indication, where a			Relevant to claim No.			
A	US 2003/0091976 (BOSCHETTI et al.) 15 May 200	3 (15.05.2003), entire	1-102				
A	CHAPMAN, K. The ProteinChip Biomarker System from Ciphergen Biosystems: a novel proteomics platform for rapid biomarker discovery and validation. Biochemical Society Transactions. April 2002, Vol. 30, part 2, pages 82-87.						
A	POON et al. Comprehensive Proteomic Profiling Ide Detection of Hepatocellular Carcinoma and Its Subty Vol. 49, No.5, pages 752-760.	1-102					
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